```
(FILE 'HOME' ENTERED AT 14:15:35 ON 22 JUN 2005)

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:15:50 ON 22 JUN 2005
L1     20260 SEA PLU=ON  (MU(3A) OPIOID(3A) RECEPTOR)
L2       307 SEA PLU=ON  L1(10A)(SNP OR MUTAT? OR POLYMORPH? OR ALLEL?)
L3       181 DUP REM L2 (126 DUPLICATES REMOVED)
L4        10 SEA PLU=ON  L3 AND (INSERTION OR DELETION)
              D TI 1-10
              D IBIB AB 9
              D IBIB AB 8
              D BIB AB 2


     FILE 'STNGUIDE' ENTERED AT 14:18:53 ON 22 JUN 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:20:15 ON 22 JUN 2005
              D IBIB AB 1


     FILE 'STNGUIDE' ENTERED AT 14:20:15 ON 22 JUN 2005
L5         0 SEA PLU=ON  L1 AND (SERINE OR PROLINE OR THREONINE OR GLYCINE)


     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:21:09 ON 22 JUN 2005
L6       635 SEA PLU=ON  L5
L7       307 SEA PLU=ON  L1(10A)(SNP OR MUTAT? OR POLYMORPH? OR ALLEL?)
L8         1 SEA PLU=ON  L6 AND ((SERINE(4A) PROLINE) OR (SER23? OR
              SER42?))
              D TI 1
L9         1 SEA PLU=ON  L1 AND T67?
              D TU'
L10        1 SEA PLU=ON  L1 AND T124?
L11        1 SEA PLU=ON  L1 AND C153?
L12        1 SEA PLU=ON  L1 AND G174?
L13      212 SEA PLU=ON  L1 AND (SNP OR MUTAT? OR POLYMORPH? OR ALLEL?)/TI
L14      114 DUP REM L13 (98 DUPLICATES REMOVED)
              D TI 1-114
              D IBIB AB 1

     FILE 'STNGUIDE' ENTERED AT 14:26:17 ON 22 JUN 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:29:25 ON 22 JUN 2005
              D IBIB AB 5 6 10 12 14 16 27-31 37 41

     FILE 'STNGUIDE' ENTERED AT 14:29:26 ON 22 JUN 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:33:41 ON 22 JUN 2005
              D IBIB AB 43 48 49 52 60 63 66 67

     FILE 'STNGUIDE' ENTERED AT 14:33:41 ON 22 JUN 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:45:07 ON 22 JUN 2005
              D IBIB AB 68 72 74 76 79 80 81 82 83 84 87 88 89

     FILE 'STNGUIDE' ENTERED AT 14:45:08 ON 22 JUN 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:00:40 ON 22 JUN 2005
              D IBIB AB 93 96 97 99 100 101

     FILE 'STNGUIDE' ENTERED AT 15:00:41 ON 22 JUN 2005

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:05:52 ON 22 JUN 2005
              D IBIB AB 104 109

     FILE 'STNGUIDE' ENTERED AT 15:05:53 ON 22 JUN 2005
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Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1374	mu with opioid	US-PGPUB; USPAT	OR	ON	2005/06/22 12:28
L2	31	l1 same (polymorph$5 snp mutation mutated)	US-PGPUB; USPAT	OR	ON	2005/06/22 12:29

From:	Switzer, Juliet
Sent:	Wednesday, June 22, 2005 9:52 AM
To:	STIC-Biotech/ChemLib
Subject:	FW: please search

Will you please update me as to the status of this rush search request?
Thanks.
Juliet

-----Original Message-----

From:	Chan, Christina
Sent:	Tuesday, June 14, 2005 12:34 PM
To:	Switzer, Juliet; STIC-Biotech/ChemLib
Subject:	RE: please search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From:	Switzer, Juliet
Sent:	Tuesday, June 14, 2005 11:27 AM
To:	Chan, Christina
Subject:	FW: please search

please approve the following rush search for a case due this biweek. thanks.

for US 09/883839 please search

in all GenEmbl, GenSeq, USPATS issued, PGPUBS, and EST databases   _259-299_
1. Seq ID NO 1 from nucleotide ~~47-87~~ where the nucleotide at postition 279 is a "C"
2. Seq ID NO 1 from nucleotide 104-144 where the nucleotide at postition 336 is a "A"   _316-356_
3. Seq ID NO 1 from nucleotide 133-173 where the nucleotide at postition 365 is a "T"   _345-385_
4. Seq ID NO 1 from nucleotide 154-194 where the nucleotide at postition 386 is a "A"   _366-406_
5. Seq ID NO 1 from nucleotide167-207 where there is an insertion of "GGC" immediately after nucleotide position 399.   _379-420_

PLEASE RETURN RESULTS ON DISK.
THanks.

Juliet Switzer
Art Unit 1634
phone: 571-272-0753
office: Remsen 2A61

GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 23:56:24 ; Search time 1680 Seconds
                                            (without alignments)
                                   1211.380 Million cell updates/sec

Title: US-09-883-839-1-GGC399_COPY_379_420
Perfect score: 42
Sequence: 1 acagcctgtgccctccgacc..........gcgcagtccctccatgatca 42

Scoring table: IDENTITY_NUC.
                  Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                  10: gb_ro:*
                  11: gb_sts:*
                  12: gb_sy:*
                  13: gb_un:*
                  14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   26   61.9   305   9   HSOPRMI1   AF024515 Homo sapi
  c 2   26   61.9   520 11   G53082   G53082 SHGC-84785
     3   26   61.9   1182   6   AX280923   AX280923 Sequence
     4   26   61.9   1203   6   AX280921   AX280921 Sequence

	5	26	61.9	1203	9	AF286024	AF286024 Macaca mu
	6	26	61.9	1203	9	AY521028	AY521028 Homo sapi
	7	26	61.9	1293	9	BC074927	BC074927 Homo sapi
	8	26	61.9	1388	9	AY036623	AY036623 Homo sapi
	9	26	61.9	1399	9	AY038989	AY038989 Macaca fa
	10	26	61.9	1464	9	AY036622	AY036622 Homo sapi
	11	26	61.9	1468	9	AY364230	AY364230 Homo sapi
	12	26	61.9	1610	6	AR106017	AR106017 Sequence
	13	26	61.9	1610	9	HUMOPIOIDA	L29301 Homo sapien
	14	26	61.9	2150	6	CQ725069	CQ725069 Sequence
	15	26	61.9	2160	6	AR162044	AR162044 Sequence
	16	26	61.9	2162	6	A87781	A87781 Sequence 7
	17	26	61.9	2162	6	AR181331	AR181331 Sequence
	18	26	61.9	2162	6	AR182295	AR182295 Sequence
	19	26	61.9	2162	6	AR270816	AR270816 Sequence
	20	26	61.9	2162	6	AR301230	AR301230 Sequence
	21	26	61.9	2162	6	AX548900	AX548900 Sequence
	22	26	61.9	2162	9	HUMMOR1X	L25119 Human Mu op
	23	26	61.9	83889	9	AY587764	AY587764 Homo sapi
C	24	26	61.9	96310	9	AL136444	AL136444 Human DNA
	25	26	61.9	182048	2	AC027439	AC027439 Homo sapi
C	26	26	61.9	182383	2	AC021745	AC021745 Homo sapi
C	27	25	59.5	200627	2	AC019225	AC019225 Homo sapi
	28	24.4	58.1	1473	9	HSU12569	U12569 Human mu op
	29	24.4	58.1	287437	2	AC123352	AC123352 Rattus no
C	30	24.2	57.6	226013	2	AC073680	AC073680 Mus muscu
C	31	24	57.1	36688	1	AY046057	AY046057 Escherich
	32	23.8	56.7	2243	6	AX402958	AX402958 Sequence
	33	23.8	56.7	4299	9	AK122591	AK122591 Homo sapi
C	34	23.8	56.7	106323	9	AL513477	AL513477 Human DNA
C	35	23.4	55.7	64459	9	AL353149	AL353149 Human DNA
	36	23.4	55.7	148290	9	AL359199	AL359199 Human DNA
C	37	23.4	55.7	165917	9	AL356073	AL356073 Human DNA
	38	23.4	55.7	177303	2	AC026576	AC026576 Homo sapi
	39	23.4	55.7	201269	2	AP001849	AP001849 Homo sapi
C	40	23.4	55.7	202114	2	BX957272	BX957272 Danio rer
C	41	23.2	55.2	299450	1	AP005938	AP005938 Bradyrhiz
	42	23	54.8	116115	8	AF546189	AF546189 Contiguou
C	43	23	54.8	149632	2	AC116692	AC116692 Mus muscu
	44	23	54.8	164294	2	AC148910	AC148910 Otolemur
C	45	23	54.8	175543	2	AC073378	AC073378 Homo sapi

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 20:32:29 ; Search time 433 Seconds
                                          (without alignments)
                                          574.201 Million cell updates/sec

Title: US-09-883-839-1-GGC399_COPY_379_420
Perfect score: 42
Sequence: 1 acagcctgtgccctccgacc.........gcgcagtccctccatgatca 42

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
c 1	26	61.9	178	12	ACH81134	Ach81134 Human gen
c 2	26	61.9	593	12	ACH67429	Ach67429 Human gen
3	26	61.9	1182	5	ABI98013	Abi98013 Non-endog
4	26	61.9	1200	13	ADR44830	Adr44830 Human HUM
5	26	61.9	1200	13	ADR44837	Adr44837 HUMOR mut
6	26	61.9	1203	5	ABI98012	Abi98012 Non-endog
7	26	61.9	1239	6	ABS54814	Abs54814 cDNA enco
8	26	61.9	1245	6	ABS54813	Abs54813 cDNA enco
9	26	61.9	1388	10	ADG42251	Adg42251 Mu-opioid

10	26	61.9	1431	6	ABS54812	Abs54812 cDNA enco
11	26	61.9	1464	10	ADG42250	Adg42250 Mu-opioid
12	26	61.9	1610	2	AAQ89226	Aaq89226 Human mu
13	26	61.9	1610	3	AAA59503	Aaa59503 cDNA enco
14	26	61.9	1610	13	ADR44881	Adr44881 Human mu-
15	26	61.9	2149	6	ABS54815	Abs54815 cDNA enco
16	26	61.9	2160	2	AAQ93102	Aaq93102 Human mu
17	26	61.9	2162	2	AAV61995	Aav61995 Human mu-
18	26	61.9	2162	2	AAV61986	Aav61986 Human mu-
19	26	61.9	2162	2	AAV61991	Aav61991 Human mu-
20	26	61.9	2162	2	AAV61988	Aav61988 Human mu-
21	26	61.9	2162	2	AAV61984	Aav61984 Human mu-
22	26	61.9	2162	2	AAV61994	Aav61994 Human mu-
23	26	61.9	2162	2	AAV61987	Aav61987 Human mu-
24	26	61.9	2162	2	AAV61992	Aav61992 Human mu-
25	26	61.9	2162	2	AAV61990	Aav61990 Human mu-
26	26	61.9	2162	2	AAV61993	Aav61993 Human mu-
27	26	61.9	2162	2	AAV61985	Aav61985 Human mu-
28	26	61.9	2162	2	AAV61989	Aav61989 Human mu-
29	26	61.9	2162	3	AAZ88470	Aaz88470 Human mu
30	26	61.9	2162	6	ABK14953	Abk14953 Human mu
31	26	61.9	2162	8	ABZ42697	Abz42697 Human opi
32	26	61.9	2162	10	ADC21534	Adc21534 Human DNA
33	26	61.9	2162	10	ACA56781	Aca56781 Human sig
34	26	61.9	2162	12	ADI56577	Adi56577 Human pol
35	26	61.9	2162	12	ADO30013	Ado30013 Human GPC
36	26	61.9	2279	8	AAD51226	Aad51226 Human REM
37	26	61.9	9426	13	ADR44835	Adr44835 FIV opioi
c 38	26	61.9	9569	13	ADR44842	Adr44842 FIV-NSE-H
39	26	61.9	10472	13	ADR44876	Adr44876 Plasmid p
40	24.4	58.1	1176	8	AAD50855	Aad50855 Human mu
41	24.4	58.1	1176	8	AAD50856	Aad50856 Human mod
42	24.4	58.1	1197	8	AAD50857	Aad50857 Human mod
43	24.4	58.1	1473	6	ABS54816	Abs54816 cDNA enco
44	23.8	56.7	2243	6	ABA94696	Aba94696 Human lip
45	23.8	56.7	4635	6	AAD39663	Aad39663 Human pho

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 01:09:40 ; Search time 128 Seconds
                                           (without alignments)
                                           536.903 Million cell updates/sec

Title: US-09-883-839-1-GGC399_COPY_379_420
Perfect score: 42
Sequence: 1 acagcctgtgccctccgacc..........gcgcagtccctccatgatca 42

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
      1   26   61.9   1182 4   US-09-826-509-546   Sequence 546, App
      2   26   61.9   1203 4   US-09-826-509-544   Sequence 544, App
      3   26   61.9   1610 3   US-08-889-108-7   Sequence 7, Appli
      4   26   61.9   1610 5   PCT-US94-10358-7   Sequence 7, Appli
      5   26   61.9   2160 3   US-08-188-275A-1   Sequence 1, Appli
      6   26   61.9   2162 3   US-09-351-198-1   Sequence 1, Appli
      7   26   61.9   2162 3   US-09-113-426-1   Sequence 1, Appli
      8   26   61.9   2162 4   US-09-016-434-1379   Sequence 1379, Ap
      9   26   61.9   2162 4   US-09-355-709C-7   Sequence 7, Appli
     10   23   54.8   1227 4   US-09-902-540-4139   Sequence 4139, Ap
C   11   23   54.8   18469 4   US-09-902-540-1205   Sequence 1205, Ap
C   12   22.8   54.3 109159 4   US-09-949-016-14169   Sequence 14169, A
C   13   22.8   54.3 109159 4   US-09-949-016-14170   Sequence 14170, A
     14   22.4   53.3   1334 4   US-09-761-962A-3   Sequence 3, Appli
     15   22.4   53.3   1346 4   US-09-761-962A-12   Sequence 12, Appl
     16   22.4   53.3   1365 4   US-09-761-962A-11   Sequence 11, Appl

	17	22.4	53.3	1423	4	US-09-761-962A-1	Sequence 1, Appli
	18	22.4	53.3	1542	4	US-09-761-962A-4	Sequence 4, Appli
	19	22.4	53.3	1610	4	US-09-761-962A-16	Sequence 16, Appl
	20	22.4	53.3	1618	3	US-08-889-108-1	Sequence 1, Appli
	21	22.4	53.3	1618	3	US-08-889-108-3	Sequence 3, Appli
	22	22.4	53.3	1618	3	US-08-120-601B-1	Sequence 1, Appli
	23	22.4	53.3	1618	3	US-08-120-601B-3	Sequence 3, Appli
	24	22.4	53.3	1618	5	PCT-US94-10358-1	Sequence 1, Appli
	25	22.4	53.3	1618	5	PCT-US94-10358-3	Sequence 3, Appli
	26	22.4	53.3	1729	4	US-09-761-962A-9	Sequence 9, Appli
	27	22.4	53.3	1981	3	US-08-387-707-15	Sequence 15, Appl
	28	22.4	53.3	1981	3	US-08-405-271A-15	Sequence 15, Appl
	29	22.4	53.3	2045	4	US-09-761-962A-10	Sequence 10, Appl
	30	22.4	53.3	2135	3	US-08-430-286A-1	Sequence 1, Appli
	31	22.4	53.3	2229	4	US-09-214-904-1	Sequence 1, Appli
c	32	22.4	53.3	29559	4	US-09-902-540-1254	Sequence 1254, Ap
	33	22.2	52.9	8147	3	US-09-514-247A-9	Sequence 9, Appli
	34	21.8	51.9	1209	4	US-09-252-991A-13620	Sequence 13620, A
c	35	21.6	51.4	265038	4	US-09-949-016-15779	Sequence 15779, A
c	36	21.4	51.0	601	4	US-09-949-016-33296	Sequence 33296, A
c	37	21.4	51.0	601	4	US-09-949-016-46379	Sequence 46379, A
	38	21.4	51.0	1542	4	US-09-489-039A-2074	Sequence 2074, Ap
c	39	21.4	51.0	2433	4	US-09-902-540-5148	Sequence 5148, Ap
	40	21.4	51.0	11465	4	US-09-949-016-13842	Sequence 13842, A
c	41	21.4	51.0	16063	3	US-09-801-052-3	Sequence 3, Appli
c	42	21.4	51.0	16063	4	US-10-020-121-3	Sequence 3, Appli
c	43	21.4	51.0	57559	4	US-09-949-016-13077	Sequence 13077, A
c	44	21.4	51.0	57560	4	US-09-949-016-12536	Sequence 12536, A
	45	21	50.0	2637	3	US-09-735-934A-1	Sequence 1, Appli

Run on: June 23, 2005, 01:41:45 ; Search time 4346 Seconds
                                          (without alignments)
                                          60.405 Million cell updates/sec

Title: US-09-883-839-1-GGC399_COPY_379_420
Perfect score: 42
Sequence: 1 acagcctgtgccctccgacc..........gcgcagtccctccatgatca 42

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
            1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
            2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
            3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
            4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
            5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
            6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
            7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
            8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
            9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
           10:   /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
           11:   /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
           12:   /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
           13:   /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
           14:   /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
           15:   /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
           16:   /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
           17:   /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
           18:   /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
           19:   /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
           20:   /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
           21:   /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
           22:   /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
           23:   /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
           24:   /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
           25:   /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
           26:   /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                          %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	38.8	92.4	2165	11	US-09-883-839-9	Sequence 9, Appli
c	2	26	61.9	178	16	US-10-029-386-14329	Sequence 14329, A
	3	26	61.9	374	19	US-10-767-701-24666	Sequence 24666, A
c	4	26	61.9	593	16	US-10-029-386-624	Sequence 624, App
	5	26	61.9	1182	10	US-09-826-509-546	Sequence 546, App
	6	26	61.9	1182	21	US-10-925-095-546	Sequence 546, App
	7	26	61.9	1203	10	US-09-826-509-544	Sequence 544, App
	8	26	61.9	1203	21	US-10-925-095-544	Sequence 544, App
	9	26	61.9	1239	14	US-10-080-917-10	Sequence 10, Appl
	10	26	61.9	1245	14	US-10-080-917-8	Sequence 8, Appli
	11	26	61.9	1388	14	US-10-185-083-26	Sequence 26, Appl
	12	26	61.9	1431	14	US-10-080-917-6	Sequence 6, Appli
	13	26	61.9	1464	14	US-10-185-083-25	Sequence 25, Appl
	14	26	61.9	2149	14	US-10-080-917-12	Sequence 12, Appl
	15	26	61.9	2162	11	US-09-883-839-1	Sequence 1, Appli
	16	26	61.9	2162	11	US-09-883-839-3	Sequence 3, Appli
	17	26	61.9	2162	11	US-09-883-839-5	Sequence 5, Appli
	18	26	61.9	2162	11	US-09-883-839-7	Sequence 7, Appli
	19	26	61.9	2162	15	US-10-225-567A-185	Sequence 185, App
	20	26	61.9	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	21	26	61.9	2162	21	US-10-500-050-1	Sequence 1, Appli
	22	26	61.9	2279	21	US-10-477-714-33	Sequence 33, Appl
	23	24.4	58.1	1176	10	US-09-935-061-11	Sequence 11, Appl
	24	24.4	58.1	1176	10	US-09-935-061-13	Sequence 13, Appl
	25	24.4	58.1	1176	19	US-10-692-071-11	Sequence 11, Appl
	26	24.4	58.1	1176	19	US-10-692-071-13	Sequence 13, Appl
	27	24.4	58.1	1197	10	US-09-935-061-15	Sequence 15, Appl
	28	24.4	58.1	1197	19	US-10-692-071-15	Sequence 15, Appl
	29	24.4	58.1	1473	14	US-10-080-917-13	Sequence 13, Appl
	30	24.4	58.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	31	23.8	56.7	2243	17	US-10-332-426-10	Sequence 10, Appl
	32	23.8	56.7	4635	9	US-09-927-112-1	Sequence 1, Appli
	33	23.8	56.7	4635	19	US-10-757-262-37	Sequence 37, Appl
	34	23.8	56.7	4635	20	US-10-784-089-1	Sequence 1, Appli
	35	23.2	55.2	183	16	US-10-029-386-20989	Sequence 20989, A
	36	23.2	55.2	576	16	US-10-029-386-7289	Sequence 7289, Ap
c	37	22.8	54.3	133955	13	US-10-087-192-1984	Sequence 1984, Ap
	38	22.4	53.3	1149	9	US-09-993-844-10	Sequence 10, Appl
	39	22.4	53.3	1149	23	US-11-026-435-10	Sequence 10, Appl
	40	22.4	53.3	1332	14	US-10-185-083-22	Sequence 22, Appl
	41	22.4	53.3	1334	9	US-09-761-962-3	Sequence 3, Appli
	42	22.4	53.3	1334	15	US-10-283-300-3	Sequence 3, Appli
	43	22.4	53.3	1346	9	US-09-761-962-12	Sequence 12, Appl
	44	22.4	53.3	1346	15	US-10-283-300-12	Sequence 12, Appl
	45	22.4	53.3	1365	9	US-09-761-962-11	Sequence 11, Appl

OM nucleic - nucleic search, using sw model

Run on: June·23, 2005, 01:02:45 ; Search time 3105 Seconds
                                          (without alignments)
                                          514.879 Million cell updates/sec

Title: US-09-883-839-1-GGC399_COPY_379_420
Perfect score: 42
Sequence: 1 acagcctgtgccctccgacc.........gcgcagtccctccatgatca 42

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_gss1:*
                9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	26	61.9	256	9	CL148070	CL148070 104_327_1
2	26	61.9	374	6	CD207450	CD207450 HS1_65_G0
c 3	26	61.9	520	8	B82759	B82759 RPCI11-17K2
4	26	61.9	582	5	BP346782	BP346782 BP346782
c 5	26	61.9	590	9	CL182795	CL182795 104_394_1
6	26	61.9	750	7	CO934661	CO934661 AGENCOURT
c 7	25	59.5	245	8	AQ488720	AQ488720 RPCI-11-2
c 8	25	59.5	472	1	AA796337	AA796337 vs94f07.r
9	24.4	58.1	718	7	CO928559	CO928559 AGENCOURT
10	24.4	58.1	738	7	CO519368	CO519368 3530_1_12
11	24	57.1	160	2	BE830599	BE830599 PM4-MT001
12	24	57.1	357	6	CA718094	CA718094 wdk5c.pk0
c 13	24	57.1	455	1	AI155930	AI155930 ue04c01.r

	14	23.6	56.2	957	2	BF781696	BF781696	602104218
c	15	23.4	55.7	197	9	CE504966	CE504966	tigr-gss-
c	16	23.4	55.7	772	9	BX201388	BX201388	Danio rer
c	17	23	54.8	677	9	AG080653	AG080653	Pan trogl
c	18	22.8	54.3	568	6	CD218844	CD218844	pgrln.pk0
c	19	22.8	54.3	606	6	CB581349	CB581349	AMGNNUC:N
c	20	22.8	54.3	608	6	CB580912	CB580912	AMGNNUC:N
	21	22.8	54.3	620	1	AU129390	AU129390	AU129390
	22	22.8	54.3	724	8	BZ211678	BZ211678	CH230-391
c	23	22.8	54.3	748	5	BU226839	BU226839	603401427
	24	22.8	54.3	865	8	BZ213735	BZ213735	CH230-294
c	25	22.8	54.3	869	7	CV109334	CV109334	AGENCOURT
c	26	22.8	54.3	891	8	BZ207785	BZ207785	CH230-475
	27	22.6	53.8	430	5	BY393833	BY393833	BY393833
c	28	22.6	53.8	651	6	BY752477	BY752477	BY752477
c	29	22.6	53.8	749	4	BM047936	BM047936	603619007
c	30	22.4	53.3	335	8	CC177529	CC177529	ZMMBBc030
c	31	22.4	53.3	348	1	AI812096	AI812096	tw77b12.x
	32	22.4	53.3	368	8	BZ374359	BZ374359	ie24a06.g
c	33	22.4	53.3	394	2	AW407892	AW407892	UI-HF-BM0
	34	22.4	53.3	421	4	BM382340	BM382340	MEST548-B
c	35	22.4	53.3	448	6	CB142408	CB142408	K-EST0196
c	36	22.4	53.3	480	6	CD630805	CD630805	55094313H
	37	22.4	53.3	493	5	BU431017	BU431017	UI-HF-BN0
c	38	22.4	53.3	501	7	CN355553	CN355553	170005999
	39	22.4	53.3	501	8	AZ620231	AZ620231	1M0452E19
c	40	22.4	53.3	517	6	CA249975	CA249975	SCRUFL111
	41	22.4	53.3	523	8	AZ436573	AZ436573	1M0224E21
c	42	22.4	53.3	528	2	AW927303	AW927303	945008E07
c	43	22.4	53.3	531	5	BM953664	BM953664	952064G02
	44	22.4	53.3	554	5	BP267205	BP267205	BP267205

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 793.33 Seconds
                                          (without alignments)
                                          2504.208 Million cell updates/sec

Title: US-09-883-839-1-C279_COPY_259_299
Perfect score: 41
Sequence: 1 ccttggcgtactcaagttgc..........ccccagcacccagccccggt 41

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
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      1   39.4   96.1   305 9   HSOPRMI1   AF024515 Homo sapi
      2   39.4   96.1   1182 6   AX280923   AX280923 Sequence
      3   39.4   96.1   1203 6   AX280921   AX280921 Sequence

	4	39.4	96.1	1203	9	AY521028	AY521028 Homo sapi
	5	39.4	96.1	1293	9	BC074927	BC074927 Homo sapi
	6	39.4	96.1	1388	9	AY036623	AY036623 Homo sapi
	7	39.4	96.1	1464	9	AY036622	AY036622 Homo sapi
	8	39.4	96.1	1468	9	AY364230	AY364230 Homo sapi
	9	39.4	96.1	1473	9	HSU12569	U12569 Human mu op
	10	39.4	96.1	1610	6	AR106017	AR106017 Sequence
	11	39.4	96.1	1610	9	HUMOPIOIDA	L29301 Homo sapien
	12	39.4	96.1	2150	6	CQ725069	CQ725069 Sequence
	13	39.4	96.1	2160	6	AR162044	AR162044 Sequence
	14	39.4	96.1	2162	6	A87781	A87781 Sequence 7
	15	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	16	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	17	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	18	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	19	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	20	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	21	39.4	96.1	3759	9	AF153500	AF153500 Homo sapi
	22	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
C	23	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	24	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi
C	25	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
	26	37.8	92.2	1399	9	AY038989	AY038989 Macaca fa
C	27	36.2	88.3	520	11	G53082	G53082 SHGC-84785
	28	36.2	88.3	1203	9	AF286024	AF286024 Macaca mu
	29	29.8	72.7	1710	10	AY166606	AY166606 Cavia por
C	30	28.2	68.8	6494	6	AX346295	AX346295 Sequence
C	31	28.2	68.8	6494	6	AX348524	AX348524 Sequence
	32	25.2	61.5	241295	2	AC130270	AC130270 Rattus no
	33	25.2	61.5	251189	2	AC126128	AC126128 Rattus no
	34	25	61.0	120936	2	AP004025	AP004025 Oryza sat
	35	25	61.0	143234	10	AC121897	AC121897 Mus muscu
	36	25	61.0	175645	8	AP004096	AP004096 Oryza sat
	37	25	61.0	181293	10	AC025786	AC025786 Mus muscu
	38	25	61.0	190165	10	AC121847	AC121847 Mus muscu
C	39	24.6	60.0	115793	9	AC104115	AC104115 Homo sapi
	40	24.6	60.0	149006	9	AC122713	AC122713 Homo sapi
	41	24.6	60.0	170803	2	AC016155	AC016155 Homo sapi
C	42	24.2	59.0	214314	2	AC121185	AC121185 Rattus no
	43	24.2	59.0	239795	2	AC130114	AC130114 Rattus no
	44	24	58.5	717	11	BV209142	BV209142 CLECSF13_
C	45	24	58.5	770	9	HSA336025	AJ336025 Homo sapi

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 279.437 Seconds
                                            (without alignments)
                                            868.566 Million cell updates/sec

Title: US-09-883-839-1-C279_COPY_259_299
Perfect score: 41
Sequence: 1 ccttggcgtactcaagttgc..........ccccagcacccagccccggt 41

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
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                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
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                   7: geneseqn2002bs:*
                   8: geneseqn2003as:*
                   9: geneseqn2003bs:*
                   10: geneseqn2003cs:*
                   11: geneseqn2003ds:*
                   12: geneseqn2004as:*
                   13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description
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c 1   39.4   96.1   593 12   ACH67429   Ach67429 Human gen
   2   39.4   96.1   1176   8   AAD50855   Aad50855 Human mu
   3   39.4   96.1   1176   8   AAD50856   Aad50856 Human mod
   4   39.4   96.1   1182   5   ABI98013   Abi98013 Non-endog
   5   39.4   96.1   1197   8   AAD50857   Aad50857 Human mod

	6	39.4	96.1	1200	13	ADR44830	Adr44830 Human HUM
	7	39.4	96.1	1200	13	ADR44837	Adr44837 HUMOR mut
	8	39.4	96.1	1203	5	ABI98012	Abi98012 Non-endog
	9	39.4	96.1	1245	6	ABS54813	Abs54813 cDNA enco
	10	39.4	96.1	1388	10	ADG42251	Adg42251 Mu-opioid
	11	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco
	12	39.4	96.1	1464	10	ADG42250	Adg42250 Mu-opioid
	13	39.4	96.1	1473	6	ABS54816	Abs54816 cDNA enco
	14	39.4	96.1	1610	2	AAQ89226	Aaq89226 Human mu
	15	39.4	96.1	1610	3	AAA59503	Aaa59503 cDNA enco
	16	39.4	96.1	1610	13	ADR44881	Adr44881 Human mu-
	17	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco
	18	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
	19	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-
	20	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-
	21	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
	22	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
	23	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
	24	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
	25	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
	26	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
	27	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
	28	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
	29	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
	30	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
	31	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
	32	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
	33	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
	34	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
	35	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
	36	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
	37	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
	38	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
	39	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
C	40	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
	41	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
C	42	28.2	68.8	6494	6	ABL33393	Abl33393 Human imm
C	43	28.2	68.8	6494	6	AAD28391	Aad28391 Human che
C	44	25	61.0	73148	12	ADQ97837	Adq97837 Mouse can
	45	24	58.5	1149	6	ABX13057	Abx13057 Human MOR

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 81.4029 Seconds
                                             (without alignments)
                                             824.139 Million cell updates/sec

Title: .   US-09-883-839-1-C279_COPY_259_299
Perfect score: 41
Sequence: 1 ccttggcgtactcaagttgc..........ccccagcacccagccccggt 41

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                          %
Result   Query
   No.   Score   Match Length DB ID   Description
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     1   39.4   96.1   1182   4 US-09-826-509-546   Sequence 546, App
     2   39.4   96.1   1203   4 US-09-826-509-544   Sequence 544, App
     3   39.4   96.1   1610   3 US-08-889-108-7   Sequence 7, Appli
     4   39.4   96.1   1610   5 PCT-US94-10358-7   Sequence 7, Appli
     5   39.4   96.1   2160   3 US-08-188-275A-1   Sequence 1, Appli
     6   39.4   96.1   2162   3 US-09-351-198-1   Sequence 1, Appli
     7   39.4   96.1   2162   3 US-09-113-426-1   Sequence 1, Appli
     8   39.4   96.1   2162   4 US-09-016-434-1379   Sequence 1379, Ap
     9   39.4   96.1   2162   4 US-09-355-709C-7   Sequence 7, Appli
    10   24   58.5   1618   3 US-08-889-108-1   Sequence 1, Appli
    11   24   58.5   1618   3 US-08-889-108-3   Sequence 3, Appli
    12   24   58.5   1618   3 US-08-120-601B-1   Sequence 1, Appli

	13	24	58.5	1618	3	US-08-120-601B-3	Sequence 3, Appli
	14	24	58.5	1618	5	PCT-US94-10358-1	Sequence 1, Appli
	15	24	58.5	1618	5	PCT-US94-10358-3	Sequence 3, Appli
	16	24	58.5	2135	3	US-08-430-286A-1	Sequence 1, Appli
	17	22.4	54.6	1334	4	US-09-761-962A-3	Sequence 3, Appli
	18	22.4	54.6	1346	4	US-09-761-962A-12	Sequence 12, Appl
	19	22.4	54.6	1365	4	US-09-761-962A-11	Sequence 11, Appl
	20	22.4	54.6	1423	4	US-09-761-962A-1	Sequence 1, Appli
	21	22.4	54.6	1542	4	US-09-761-962A-4	Sequence 4, Appli
	22	22.4	54.6	1610	4	US-09-761-962A-16	Sequence 16, Appl
	23	22.4	54.6	1729	4	US-09-761-962A-9	Sequence 9, Appli
	24	22.4	54.6	1981	3	US-08-387-707-15	Sequence 15, Appl
	25	22.4	54.6	1981	3	US-08-405-271A-15	Sequence 15, Appl
	26	22.4	54.6	2045	4	US-09-761-962A-10	Sequence 10, Appl
	27	21.2	51.7	746	4	US-10-237-551-219	Sequence 219, App
	28	21.2	51.7	823	4	US-10-237-551-220	Sequence 220, App
	29	21.2	51.7	3591	4	US-10-237-551-191	Sequence 191, App
	30	21.2	51.7	3591	4	US-10-237-551-221	Sequence 221, App
	31	21.2	51.7	13579	4	US-09-902-540-1101	Sequence 1101, Ap
C	32	21.2	51.7	154746	4	US-09-827-688-8	Sequence 8, Appli
	33	21	51.2	601	4	US-09-949-016-202775	Sequence 202775,
	34	21	51.2	601	4	US-09-949-016-202776	Sequence 202776,
	35	21	51.2	601	4	US-09-949-016-202777	Sequence 202777,
C	36	21	51.2	4200	4	US-09-949-016-5718	Sequence 5718, Ap
C	37	21	51.2	4201	4	US-09-949-016-445	Sequence 445, App
C	38	21	51.2	14207	4	US-09-949-016-12187	Sequence 12187, A
C	39	21	51.2	14207	4	US-09-949-016-17460	Sequence 17460, A
	40	21	51.2	29954	4	US-09-949-016-13808	Sequence 13808, A
	41	21	51.2	31040	4	US-09-949-016-12383	Sequence 12383, A
C	42	21	51.2	41815	4	US-09-949-016-17447	Sequence 17447, A
C	43	20.8	50.7	427	4	US-09-513-999C-2453	Sequence 2453, Ap
C	44	20.8	50.7	636	4	US-09-252-991A-11982	Sequence 11982, A
	45	20.8	50.7	639	4	US-09-902-540-5899	Sequence 5899, Ap

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:19 ; Search time 380.544 Seconds
                                      (without alignments)
                                      668.805 Million cell updates/sec

Title: US-09-883-839-1-C279_COPY_259_299
Perfect score: 41
Sequence: 1 ccttggcgtactcaagttgc..........ccccagcacccagccccggt 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	41	100.0	2162	11	US-09-883-839-3	Sequence 3, Appli
c	2	39.4	96.1	593	16	US-10-029-386-624	Sequence 624, App
	3	39.4	96.1	1176	10	US-09-935-061-11	Sequence 11, Appl
	4	39.4	96.1	1176	10	US-09-935-061-13	Sequence 13, Appl
	5	39.4	96.1	1176	19	US-10-692-071-11	Sequence 11, Appl
	6	39.4	96.1	1176	19	US-10-692-071-13	Sequence 13, Appl
	7	39.4	96.1	1182	10	US-09-826-509-546	Sequence 546, App
	8	39.4	96.1	1182	21	US-10-925-095-546	Sequence 546, App
	9	39.4	96.1	1197	10	US-09-935-061-15	Sequence 15, Appl
	10	39.4	96.1	1197	19	US-10-692-071-15	Sequence 15, Appl
	11	39.4	96.1	1203	10	US-09-826-509-544	Sequence 544, App
	12	39.4	96.1	1203	21	US-10-925-095-544	Sequence 544, App
	13	39.4	96.1	1245	14	US-10-080-917-8	Sequence 8, Appli
	14	39.4	96.1	1388	14	US-10-185-083-26	Sequence 26, Appl
	15	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	16	39.4	96.1	1464	14	US-10-185-083-25	Sequence 25, Appl
	17	39.4	96.1	1473	14	US-10-080-917-13	Sequence 13, Appl
	18	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	19	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	20	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	21	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	22	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	23	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	24	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	25	39.4	96.1	2162	21	US-10-500-050-1	Sequence 1, Appli
	26	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
	27	39.4	96.1	2279	21	US-10-477-714-33	Sequence 33, Appl
c	28	28.2	68.8	6494	15	US-10-311-455-1366	Sequence 1366, Ap
	29	24	58.5	1149	9	US-09-993-844-10	Sequence 10, Appl
	30	24	58.5	1149	23	US-11-026-435-10	Sequence 10, Appl
	31	24	58.5	1239	14	US-10-080-917-10	Sequence 10, Appl
	32	24	58.5	1618	10	US-09-841-720-1	Sequence 1, Appli
	33	24	58.5	1618	10	US-09-841-720-3	Sequence 3, Appli
c	34	23.6	57.6	654	13	US-10-027-632-128080	Sequence 128080,
c	35	23.6	57.6	654	17	US-10-027-632-128080	Sequence 128080,
c	36	23.6	57.6	884	13	US-10-027-632-128079	Sequence 128079,
c	37	23.6	57.6	884	17	US-10-027-632-128079	Sequence 128079,
	38	23.6	57.6	23825	17	US-10-085-117-166	Sequence 166, App
c	39	23.4	57.1	2245	19	US-10-437-963-33929	Sequence 33929, A
	40	23.2	56.6	3787	10	US-09-930-213-284	Sequence 284, App
c	41	22.6	55.1	3241	13	US-10-027-632-115314	Sequence 115314,
c	42	22.6	55.1	3241	17	US-10-027-632-115314	Sequence 115314,
c	43	22.4	54.6	591	19	US-10-437-963-80051	Sequence 80051, A
	44	22.4	54.6	1332	14	US-10-185-083-22	Sequence 22, Appl
	45	22.4	54.6	1334	9	US-09-761-962-3	Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 2429.15 Seconds
                                              (without alignments)
                                              642.461 Million cell updates/sec

Title: US-09-883-839-1-C279_COPY_259_299
Perfect score: 41
Sequence: 1 ccttggcgtactcaagttgc..........ccccagcacccagccccggt 41

Scoring table: IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                    1: gb_est1:*
                    2: gb_est2:*
                    3: gb_htc:*
                    4: gb_est3:*
                    5: gb_est4:*
                    6: gb_est5:*
                    7: gb_est6:*
                    8: gb_gss1:*
                    9: gb_gss2:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
        1   39.4   96.1   582   5   BP346782   BP346782 BP346782
        2   39.4   96.1   750   7   CO934661   CO934661 AGENCOURT
c   3   36.2   88.3   520   8   B82759   B82759 RPCI11-17K2
        4   36.2   88.3   718   7   CO928559   CO928559 AGENCOURT
c   5   29.8   72.7   525   8   AQ767579   AQ767579 HS_3206_A
c   6   23.6   57.6   334   1   AA372004   AA372004 EST84101
c   7   23.6   57.6   534   2   BE503927   BE503927 hz52a02.x
        8   23.6   57.6   792   5   BU525431   BU525431 AGENCOURT
        9   23.4   57.1   507   5   BY417585   BY417585 BY417585

c	10	23.4	57.1	548	1	AA196212	AA196212	zp98a04.r
	11	23.2	56.6	252	4	BM480972	BM480972	532708 MA
	12	23.2	56.6	637	7	CN529326	CN529326	UI-M-HQ0-
	13	23.2	56.6	666	2	BB620973	BB620973	BB620973
	14	23.2	56.6	677	7	CF749574	CF749574	UI-M-HJ0-
c	15	23.2	56.6	747	7	CK847349	CK847349	969981 MA
	16	23.2	56.6	765	7	CN539280	CN539280	UI-M-HU0-
	17	23.2	56.6	778	5	BU613885	BU613885	UI-M-EW0-
	18	23.2	56.6	791	7	CO431610	CO431610	UI-M-HX0-
	19	23.2	56.6	801	7	CF739765	CF739765	UI-M-HD0-
	20	23.2	56.6	925	5	BU523452	BU523452	AGENCOURT
	21	23.2	56.6	967	5	BU503530	BU503530	AGENCOURT
c	22	23.2	56.6	994	7	CO726466	CO726466	ILLUMIGEN
	23	23.2	56.6	1116	5	BX364419	BX364419	BX364419
	24	23.2	56.6	3204	9	AY415718	AY415718	Mus muscu
	25	23	56.1	589	4	BM439566	BM439566	pgr1c.pk0
	26	23	56.1	598	9	CE456216	CE456216	tigr-gss-
	27	23	56.1	668	7	CO666279	CO666279	DG33-15g1
	28	23	56.1	768	9	CC579968	CC579968	CH240_374
c	29	23	56.1	866	5	BQ879724	BQ879724	AGENCOURT
	30	22.6	55.1	525	6	CA817080	CA817080	CA12EI202
c	31	22.6	55.1	603	2	BB659244	BB659244	BB659244
c	32	22.6	55.1	624	5	BU703269	BU703269	UI-M-FD0-
c	33	22.6	55.1	628	7	CO102348	CO102348	GR__Eb002
c	34	22.6	55.1	661	6	BY745782	BY745782	BY745782
c	35	22.6	55.1	702	7	CO109781	CO109781	GR__Eb004
	36	22.6	55.1	1029	9	CNS0101V	AL098413	Drosophil
c	37	22.4	54.6	343	6	C82449	C82449	C82449 rabb
	38	22.4	54.6	343	6	C83305	C83305	C83305 rabb
	39	22.4	54.6	407	5	BY004651	BY004651	BY004651
c	40	22.4	54.6	441	9	AB060342	AB060342	Homo sapi
	41	22.4	54.6	505	7	CO615856	CO615856	DG9-15011
	42	22.4	54.6	526	7	CO681394	CO681394	DG11-129h
	43	22.4	54.6	540	7	CK619447	CK619447	mk24c05.y
	44	22.4	54.6	560	7	CO697082	CO697082	DG32-108i
	45	22.4	54.6	581	7	CO705739	CO705739	DG32-3o23

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 793.33 Seconds
                                           (without alignments)
                                           2504.208 Million cell updates/sec

Title: US-09-883-839-1-A336_COPY_316_356
Perfect score: 41
Sequence: 1 cccacttagatggcaacctg..........ccgacccatgcggtccgaac 41

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                   1: gb_ba:*
                   2: gb_htg:*
                   3: gb_in:*
                   4: gb_om:*
                   5: gb_ov:*
                   6: gb_pat:*
                   7: gb_ph:*
                   8: gb_pl:*
                   9: gb_pr:*
                   10: gb_ro:*
                   11: gb_sts:*
                   12: gb_sy:*
                   13: gb_un:*
                   14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description
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      1   39.4   96.1   305   9   HSOPRMI1   AF024515 Homo sapi
  c   2   39.4   96.1   520 11   G53082   G53082 SHGC-84785
      3   39.4   96.1   1182   6   AX280923   AX280923 Sequence
      4   39.4   96.1   1203   6   AX280921   AX280921 Sequence

	5	39.4	96.1	1203	9	AF286024	AF286024 Macaca mu
	6	39.4	96.1	1203	9	AY521028	AY521028 Homo sapi
	7	39.4	96.1	1293	9	BC074927	BC074927 Homo sapi
	8	39.4	96.1	1388	9	AY036623	AY036623 Homo sapi
	9	39.4	96.1	1399	9	AY038989	AY038989 Macaca fa
	10	39.4	96.1	1464	9	AY036622	AY036622 Homo sapi
	11	39.4	96.1	1468	9	AY364230	AY364230 Homo sapi
	12	39.4	96.1	1610	6	AR106017	AR106017 Sequence
	13	39.4	96.1	1610	9	HUMOPIOIDA	L29301 Homo sapien
	14	39.4	96.1	2150	6	CQ725069	CQ725069 Sequence
	15	39.4	96.1	2160	6	AR162044	AR162044 Sequence
	16	39.4	96.1	2162	6	A87781	A87781 Sequence 7
	17	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	18	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	19	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	20	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	21	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	22	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	23	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
c	24	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	25	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi
c	26	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
	27	37.8	92.2	1415	4	BTU89677	U89677 Bos taurus
	28	37.8	92.2	1473	9	HSU12569	U12569 Human mu op
	29	36.2	88.3	1710	10	AY166606	AY166606 Cavia por
	30	35.4	86.3	3759	9	AF153500	AF153500 Homo sapi
	31	33	80.5	1332	10	AF346813	AF346813 Mus muscu
	32	33	80.5	1334	6	AR269386	AR269386 Sequence
	33	33	80.5	1334	10	AF074973	AF074973 Mus muscu
	34	33	80.5	1346	6	AR269395	AR269395 Sequence
	35	33	80.5	1346	10	AF167566	AF167566 Mus muscu
	36	33	80.5	1365	6	AR269394	AR269394 Sequence
	37	33	80.5	1365	10	AF167565	AF167565 Mus muscu
	38	33	80.5	1373	10	AY160190	AY160190 Mus muscu
	39	33	80.5	1423	6	AR269384	AR269384 Sequence
	40	33	80.5	1423	10	AF062753	AF062753 Mus muscu
	41	33	80.5	1438	10	AF346812	AF346812 Mus muscu
	42	33	80.5	1440	10	AF260306	AF260306 Mus muscu
	43	33	80.5	1440	10	AF400246	AF400246 Mus muscu
	44	33	80.5	1500	10	AF346814	AF346814 Mus muscu
	45	33	80.5	1542	6	AR269387	AR269387 Sequence

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 279.437 Seconds
                                            (without alignments)
                                            868.566 Million cell updates/sec

Title: US-09-883-839-1-A336_COPY_316_356
Perfect score: 41
Sequence: 1 cccacttagatggcaacctg..........ccgacccatgcggtccgaac 41

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002as:*
                  7: geneseqn2002bs:*
                  8: geneseqn2003as:*
                  9: geneseqn2003bs:*
                  10: geneseqn2003cs:*
                  11: geneseqn2003ds:*
                  12: geneseqn2004as:*
                  13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score Match Length DB ID   Description
     ----
c   1   39.4   96.1   593   12 ACH67429   Ach67429 Human gen
    2   39.4   96.1   1182   5 ABI98013   Abi98013 Non-endog
    3   39.4   96.1   1200   13 ADR44830   Adr44830 Human HUM
    4   39.4   96.1   1200   13 ADR44837   Adr44837 HUMOR mut
    5   39.4   96.1   1203   5 ABI98012   Abi98012 Non-endog

6	39.4	96.1	1239	6	ABS54814	Abs54814 cDNA enco
7	39.4	96.1	1245	6	ABS54813	Abs54813 cDNA enco
8	39.4	96.1	1388	10	ADG42251	Adg42251 Mu-opioid
9	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco
10	39.4	96.1	1464	10	ADG42250	Adg42250 Mu-opioid
11	39.4	96.1	1610	2	AAQ89226	Aaq89226 Human mu
12	39.4	96.1	1610	3	AAA59503	Aaa59503 cDNA enco
13	39.4	96.1	1610	13	ADR44881	Adr44881 Human mu-
14	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco
15	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
16	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-
17	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-
18	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
19	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
20	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
21	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
22	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
23	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
24	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
25	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
26	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
27	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
28	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
29	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
30	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
31	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
32	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
33	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
34	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
35	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
36	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
37	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
38	37.8	92.2	1176	8	AAD50855	Aad50855 Human mu
39	37.8	92.2	1176	8	AAD50856	Aad50856 Human mod
40	37.8	92.2	1197	8	AAD50857	Aad50857 Human mod
41	37.8	92.2	1415	13	ADR44844	Adr44844 Bovine mu
42	37.8	92.2	1473	6	ABS54816	Abs54816 cDNA enco
43	37.8	92.2	2162	2	AAV61990	Aav61990 Human mu-
44	33	80.5	1194	13	ADR44832	Adr44832 Mouse HUM
45	33	80.5	1197	12	ADO30303	Ado30303 Mouse GPC

c

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 279.437 Seconds
                                          (without alignments)
                                          868.566 Million cell updates/sec

Title: US-09-883-839-1-A336_COPY_316_356
Perfect score: 41
Sequence: 1 cccacttagatggcaacctg..........ccgacccatgcggtccgaac 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
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                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
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c   1   39.4   96.1   593 12   ACH67429   Ach67429 Human gen
    2   39.4   96.1   1182   5   ABI98013   Abi98013 Non-endog
    3   39.4   96.1   1200 13   ADR44830   Adr44830 Human HUM
    4   39.4   96.1   1200 13   ADR44837   Adr44837 HUMOR mut
    5   39.4   96.1   1203   5   ABI98012   Abi98012 Non-endog

	6	39.4	96.1	1239	6	ABS54814	Abs54814 cDNA enco
	7	39.4	96.1	1245	6	ABS54813	Abs54813 cDNA enco
	8	39.4	96.1	1388	10	ADG42251	Adg42251 Mu-opioid
	9	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco
	10	39.4	96.1	1464	10	ADG42250	Adg42250 Mu-opioid
	11	39.4	96.1	1610	2	AAQ89226	Aaq89226 Human mu
	12	39.4	96.1	1610	3	AAA59503	Aaa59503 cDNA enco
	13	39.4	96.1	1610	13	ADR44881	Adr44881 Human mu-
	14	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco
	15	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
	16	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-
	17	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-
	18	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
	19	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
	20	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
	21	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
	22	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
	23	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
	24	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
	25	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
	26	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
	27	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
	28	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
	29	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
	30	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
	31	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
	32	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
	33	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
	34	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
	35	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
c	36	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
	37	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
	38	37.8	92.2	1176	8	AAD50855	Aad50855 Human mu
	39	37.8	92.2	1176	8	AAD50856	Aad50856 Human mod
	40	37.8	92.2	1197	8	AAD50857	Aad50857 Human mod
	41	37.8	92.2	1415	13	ADR44844	Adr44844 Bovine mu
	42	37.8	92.2	1473	6	ABS54816	Abs54816 cDNA enco
	43	37.8	92.2	2162	2	AAV61990	Aav61990·Human mu-
	44	33	80.5	1194	13	ADR44832	Adr44832 Mouse HUM
	45	33	80.5	1197	12	ADO30303	Ado30303 Mouse GPC

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 81.4029 Seconds
                                          (without alignments)
                                          824.139 Million cell updates/sec

Title: US-09-883-839-1-A336_COPY_316_356
Perfect score: 41
Sequence: 1 cccacttagatggcaacctg..........ccgacccatgcggtccgaac 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
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     1   39.4   96.1 1182   4 US-09-826-509-546   Sequence 546, App
     2   39.4   96.1 1203   4 US-09-826-509-544   Sequence 544, App
     3   39.4   96.1 1610   3 US-08-889-108-7   Sequence 7, Appli
     4   39.4   96.1 1610   5 PCT-US94-10358-7   Sequence 7, Appli
     5   39.4   96.1 2160   3 US-08-188-275A-1   Sequence 1, Appli
     6   39.4   96.1 2162   3 US-09-351-198-1   Sequence 1, Appli
     7   39.4   96.1 2162   3 US-09-113-426-1   Sequence 1, Appli
     8   39.4   96.1 2162   4 US-09-016-434-1379   Sequence 1379, Ap
     9   39.4   96.1 2162   4 US-09-355-709C-7   Sequence 7, Appli
    10   33   80.5 1334   4 US-09-761-962A-3   Sequence 3, Appli
    11   33   80.5 1346   4 US-09-761-962A-12   Sequence 12, Appl
    12   33   80.5 1365   4 US-09-761-962A-11   Sequence 11, Appl

	13	33	80.5	1423	4	US-09-761-962A-1	Sequence 1, Appli
	14	33	80.5	1542	4	US-09-761-962A-4	Sequence 4, Appli
	15	33	80.5	1610	4	US-09-761-962A-16	Sequence 16, Appl
	16	33	80.5	1729	4	US-09-761-962A-9	Sequence 9, Appli
	17	33	80.5	2045	4	US-09-761-962A-10	Sequence 10, Appl
	18	33	80.5	2229	4	US-09-214-904-1	Sequence 1, Appli
	19	31.4	76.6	1618	3	US-08-889-108-1	Sequence 1, Appli
	20	31.4	76.6	1618	3	US-08-889-108-3	Sequence 3, Appli
	21	31.4	76.6	1618	3	US-08-120-601B-1	Sequence 1, Appli
	22	31.4	76.6	1618	3	US-08-120-601B-3	Sequence 3, Appli
	23	31.4	76.6	1618	5	PCT-US94-10358-1	Sequence 1, Appli
	24	31.4	76.6	1618	5	PCT-US94-10358-3	Sequence 3, Appli
	25	31.4	76.6	1981	3	US-08-387-707-15	Sequence 15, Appl
	26	31.4	76.6	1981	3	US-08-405-271A-15	Sequence 15, Appl
	27	31.4	76.6	2135	3	US-08-430-286A-1	Sequence 1, Appli
c	28	29.8	72.7	33	3	US-09-351-198-7	Sequence 7, Appli
c	29	29.8	72.7	33	3	US-09-113-426-7	Sequence 7, Appli
	30	25.8	62.9	33	3	US-09-351-198-6	Sequence 6, Appli
	31	25.8	62.9	33	3	US-09-113-426-6	Sequence 6, Appli
	32	22	53.7	549	4	US-09-328-352-1910	Sequence 1910, Ap
c	33	20.8	50.7	601	4	US-09-949-016-71020	Sequence 71020, A
c	34	20.8	50.7	91559	4	US-09-949-016-12581	Sequence 12581, A
c	35	20.8	50.7	91559	4	US-09-949-016-13701	Sequence 13701, A
c	36	20.8	50.7	276687	4	US-09-949-016-13840	Sequence 13840, A
	37	20.4	49.8	789	4	US-09-252-991A-555	Sequence 555, App
	38	20.4	49.8	825	4	US-09-252-991A-576	Sequence 576, App
	39	20.2	49.3	3295	4	US-10-101-464A-463	Sequence 463, App
c	40	20	48.8	3479	4	US-08-994-689C-3	Sequence 3, Appli
	41	20	48.8	5077	2	US-08-687-956A-22	Sequence 22, Appl
c	42	20	48.8	5276	4	US-08-994-689C-9	Sequence 9, Appli
c	43	20	48.8	7664	4	US-08-994-689C-10	Sequence 10, Appl
c	44	19.8	48.3	601	4	US-09-949-016-187883	Sequence 187883,
c	45	19.8	48.3	601	4	US-09-949-016-187884	Sequence 187884,

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:19 ; Search time 380.544 Seconds
                                            (without alignments)
                                            668.805 Million cell updates/sec

Title: US-09-883-839-1-A336_COPY_316_356
Perfect score: 41
Sequence: 1 cccacttagatggcaacctg..........ccgacccatgcggtccgaac 41

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                   1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                   2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                   3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                   4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                   5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                   6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                   7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                   8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                   9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                   10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                   11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                   12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                   13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                   14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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                   16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                   17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                   18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                   19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                   20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                   21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                   22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                   23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                   24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                   25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                   26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	41	100.0	2162	11	US-09-883-839-5	Sequence 5, Appli
c	2	39.4	96.1	593	16	US-10-029-386-624	Sequence 624, App
	3	39.4	96.1	1182	10	US-09-826-509-546	Sequence 546, App
	4	39.4	96.1	1182	21	US-10-925-095-546	Sequence 546, App
	5	39.4	96.1	1203	10	US-09-826-509-544	Sequence 544, App
	6	39.4	96.1	1203	21	US-10-925-095-544	Sequence 544, App
	7	39.4	96.1	1239	14	US-10-080-917-10	Sequence 10, Appl
	8	39.4	96.1	1245	14	US-10-080-917-8	Sequence 8, Appli
	9	39.4	96.1	1388	14	US-10-185-083-26	Sequence 26, Appl
	10	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	11	39.4	96.1	1464	14	US-10-185-083-25	Sequence 25, Appl
	12	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	13	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	14	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	15	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	16	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	17	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	18	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	19	39.4	96.1	2162	21	US-10-500-050-1	Sequence 1, Appli
	20	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
	21	39.4	96.1	2279	21	US-10-477-714-33	Sequence 33; Appl
	22	37.8	92.2	1176	10	US-09-935-061-11	Sequence 11, Appl
	23	37.8	92.2	1176	10	US-09-935-061-13	Sequence 13, Appl
	24	37.8	92.2	1176	19	US-10-692-071-11	Sequence 11, Appl
	25	37.8	92.2	1176	19	US-10-692-071-13	Sequence 13, Appl
	26	37.8	92.2	1197	10	US-09-935-061-15	Sequence 15, Appl
	27	37.8	92.2	1197	19	US-10-692-071-15	Sequence 15, Appl
	28	37.8	92.2	1473	14	US-10-080-917-13	Sequence 13, Appl
	29	33	80.5	1332	14	US-10-185-083-22	Sequence 22, Appl
	30	33	80.5	1334	9	US-09-761-962-3	Sequence 3, Appli
	31	33	80.5	1334	15	US-10-283-300-3	Sequence 3, Appli
	32	33	80.5	1346	9	US-09-761-962-12	Sequence 12, Appl
	33	33	80.5	1346	15	US-10-283-300-12	Sequence 12, Appl
	34	33	80.5	1365	9	US-09-761-962-11	Sequence 11, Appl
	35	33	80.5	1365	15	US-10-283-300-11	Sequence 11, Appl
	36	33	80.5	1373	14	US-10-185-083-51	Sequence 51, Appl
	37	33	80.5	1423	9	US-09-761-962-1	Sequence 1, Appli
	38	33	80.5	1423	15	US-10-283-300-1	Sequence 1, Appli
	39	33	80.5	1440	14	US-10-185-083-15	Sequence 15, Appl
	40	33	80.5	1542	9	US-09-761-962-4	Sequence 4, Appli
	41	33	80.5	1542	15	US-10-283-300-4	Sequence 4, Appli
	42	33	80.5	1569	14	US-10-185-083-17	Sequence 17, Appl
	43	33	80.5	1610	9	US-09-761-962-16	Sequence 16, Appl
	44	33	80.5	1610	15	US-10-283-300-16	Sequence 16, Appl
	45	33	80.5	1614	14	US-10-185-083-16	Sequence 16, Appl

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 2429.15 Seconds
                                           (without alignments)
                                           642.461 Million cell updates/sec

Title: US-09-883-839-1-A336_COPY_316_356
Perfect score: 41
Sequence: 1 cccacttagatggcaacctg..........ccgacccatgcggtccgaac 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                    SUMMARIES

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
c 1	39.4	96.1	520	8	B82759	B82759 RPCI11-17K2
2	39.4	96.1	582	5	BP346782	BP346782 BP346782
3	39.4	96.1	750	7	CO934661	CO934661 AGENCOURT
4	37.8	92.2	718	7	CO928559	CO928559 AGENCOURT
5	33	80.5	657	2	BB588668	BB588668 BB588668
6	33	80.5	2405	3	AK038389	AK038389 Mus muscu
c 7	31.4	76.6	525	8	AQ767579	AQ767579 HS_3206_A
8	23	56.1	889	4	BG849999	BG849999 1024027G0
9	22.6	55.1	827	5	BP144429	BP144429 BP144429
10	22.4	54.6	378	8	AQ664846	AQ664846 HS_5303_B
c 11	22.4	54.6	419	8	BH226890	BH226890 1006135E1
12	22.4	54.6	446	8	AQ465200	AQ465200 HS_5109_A
c 13	22.4	54.6	986	9	CNS02LJI	AL202887 Tetraodon

	14	22.2	54.1	741	9	CL398298	CL398298 ZMMBBb039
	15	22.2	54.1	987	4	BI457684	BI457684 603198115
c	16	22	53.7	663	9	CC864029	CC864029 NDL.126F1
	17	22	53.7	732	6	CD904206	CD904206 G356.112M
c	18	22	53.7	847	3	CR657183	CR657183 Tetraodon
	19	21.8	53.2	353	1	AI069902	AI069902 TENU2950
c	20	21.8	53.2	421	8	B42292	B42292 HS-1055-B1-
	21	21.8	53.2	571	4	BM516601	BM516601 kj56e03.y
	22	21.8	53.2	591	6	CA954651	CA954651 kl29g09.y
	23	21.8	53.2	1054	4	BM561778	BM561778 AGENCOURT
	24	21.6	52.7	295	2	BB081806	BB081806 BB081806
c	25	21.6	52.7	823	3	CR665956	CR665956 Tetraodon
	26	21.4	52.2	285	2	BB229933	BB229933 BB229933
c	27	21.4	52.2	364	9	CG666000	CG666000 OST455524
c	28	21.4	52.2	537	9	CG558846	CG558846 OST176883
c	29	21.4	52.2	581	7	CO716921	CO716921 DG14-33i1
c	30	21.4	52.2	759	4	BG481379	BG481379 602528734
c	31	21.4	52.2	821	5	BX695725	BX695725 BX695725
c	32	21.4	52.2	909	5	BQ893216	BQ893216 AGENCOURT
c	33	21.2	51.7	357	1	AI978258	AI978258 614042E03
	34	21.2	51.7	536	5	BX518910	BX518910 BX518910
	35	21.2	51.7	549	8	AZ387130	AZ387130 1M0146M20
	36	21.2	51.7	585	8	AZ624805	AZ624805 1M0463P18
	37	21.2	51.7	718	5	BQ442440	BQ442440 UI-M-EV0-
	38	21.2	51.7	732	7	CV014298	CV014298 TL018D02
	39	21.2	51.7	781	9	AG592805	AG592805 Mus muscu
c	40	21.2	51.7	787	9	CG036278	CG036278 PUIAK91TD
	41	21.2	51.7	800	6	CA320715	CA320715 UI-M-FW0-
c	42	21.2	51.7	850	3	CR675138	CR675138 Tetraodon
c	43	21.2	51.7	963	3	CR669582	CR669582 Tetraodon
c	44	21.2	51.7	979	3	CR669611	CR669611 Tetraodon
c	45	21.2	51.7	1004	3	CR663133	CR663133 Tetraodon

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 793.33 Seconds
                                             (without alignments)
                                             2504.208 Million cell updates/sec

Title: .   US-09-883-839-1-386A_COPY_366_406
Perfect score: 41
Sequence: 1 ctgggcgggagagacagcct..........tgccctccgaccggcagtcc 41

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                  10: gb_ro:*
                  11: gb_sts:*
                  12: gb_sy:*
                  13: gb_un:*
                  14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
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      1   39.4   96.1   305   9   HSOPRMI1   AF024515 Homo sapi
  c   2   39.4   96.1   520 11   G53082   G53082 SHGC-84785
      3   39.4   96.1   1182   6   AX280923   AX280923 Sequence
      4   39.4   96.1   1203   6   AX280921   AX280921 Sequence

	5	39.4	96.1	1203	9	AF286024	AF286024 Macaca mu
	6	39.4	96.1	1203	9	AY521028	AY521028 Homo sapi
	7	39.4	96.1	1293	9	BC074927	BC074927 Homo sapi
	8	39.4	96.1	1388	9	AY036623	AY036623 Homo sapi
	9	39.4	96.1	1399	9	AY038989	AY038989 Macaca fa
	10	39.4	96.1	1464	9	AY036622	AY036622 Homo sapi
	11	39.4	96.1	1468	9	AY364230	AY364230 Homo sapi
	12	39.4	96.1	1610	6	AR106017	AR106017 Sequence
	13	39.4	96.1	1610	9	HUMOPIOIDA	L29301 Homo sapien
	14	39.4	96.1	2150	6	CQ725069	CQ725069 Sequence
	15	39.4	96.1	2160	6	AR162044	AR162044 Sequence
	16	39.4	96.1	2162	6	A87781	A87781 Sequence 7
	17	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	18	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	19	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	20	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	21	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	22	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	23	39.4	96.1	83889	9	AY587764	AY587764 Homo sapi
C	24	39.4	96.1	96310	9	AL136444	AL136444 Human DNA
	25	39.4	96.1	182048	2	AC027439	AC027439 Homo sapi
C	26	39.4	96.1	182383	2	AC021745	AC021745 Homo sapi
	27	37.8	92.2	1473	9	HSU12569	U12569 Human mu op
	28	37.8	92.2	1881	4	AF521309	AF521309 Sus scrof
	29	37.8	92.2	1881	4	PIGMUOPR	L38645 Sus scrofa
	30	34.6	84.4	1710	10	AY166606	AY166606 Cavia por
	31	31.4	76.6	1332	10	AF346813	AF346813 Mus muscu
	32	31.4	76.6	1334	6	AR269386	AR269386 Sequence
	33	31.4	76.6	1334	10	AF074973	AF074973 Mus muscu
	34	31.4	76.6	1346	6	AR269395	AR269395 Sequence
	35	31.4	76.6	1346	10	AF167566	AF167566 Mus muscu
	36	31.4	76.6	1365	6	AR269394	AR269394 Sequence
	37	31.4	76.6	1365	10	AF167565	AF167565 Mus muscu
	38	31.4	76.6	1367	10	RNU35424	U35424 Rattus norv
	39	31.4	76.6	1373	10	AY160190	AY160190 Mus muscu
	40	31.4	76.6	1401	10	RATMOPIOID	L22455 Rat mu opio
	41	31.4	76.6	1423	6	AR269384	AR269384 Sequence
	42	31.4	76.6	1423	10	AF062753	AF062753 Mus muscu
	43	31.4	76.6	1438	10	AF346812	AF346812 Mus muscu
	44	31.4	76.6	1440	10	AF260306	AF260306 Mus muscu
	45	31.4	76.6	1440	10	AF400246	AF400246 Mus muscu

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 279.437 Seconds
                                          (without alignments)
                                          868.566 Million cell updates/sec

Title: US-09-883-839-1-386A_COPY_366_406
Perfect score: 41
Sequence: 1 ctgggcgggagagacagcct..........tgccctccgaccggcagtcc 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
    No.   Score   Match Length DB   ID   Description
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c   1   39.4   96.1   178   12   ACH81134   Ach81134 Human gen
c   2   39.4   96.1   593   12   ACH67429   Ach67429 Human gen
    3   39.4   96.1   1182   5   ABI98013   Abi98013 Non-endog
    4   39.4   96.1   1200   13   ADR44830   Adr44830 Human HUM
    5   39.4   96.1   1200   13   ADR44837   Adr44837 HUMOR mut
    6   39.4   96.1   1203   5   ABI98012   Abi98012 Non-endog
    7   39.4   96.1   1239   6   ABS54814   Abs54814 cDNA enco
    8   39.4   96.1   1245   6   ABS54813   Abs54813 cDNA enco
    9   39.4   96.1   1388   10   ADG42251   Adg42251 Mu-opioid

10	39.4	96.1	1431	6	ABS54812	Abs54812 cDNA enco
11	39.4	96.1	1464	10	ADG42250	Adg42250 Mu-opioid
12	39.4	96.1	1610	2	AAQ89226	Aaq89226 Human mu
13	39.4	96.1	1610	3	AAA59503	Aaa59503 cDNA enco
14	39.4	96.1	1610	13	ADR44881	Adr44881 Human mu-
15	39.4	96.1	2149	6	ABS54815	Abs54815 cDNA enco
16	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
17	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-
18	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-
19	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
20	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
21	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
22	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
23	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
24	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
25	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
26	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
27	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
28	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
29	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
30	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
31	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
32	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
33	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
34	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
35	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
36	39.4	96.1	2279	8	AAD51226	Aad51226 Human REM
37	39.4	96.1	9426	13	ADR44835	Adr44835 FIV opioi
c 38	39.4	96.1	9569	13	ADR44842	Adr44842 FIV-NSE-H
39	39.4	96.1	10472	13	ADR44876	Adr44876 Plasmid p
40	37.8	92.2	1176	8	AAD50855	Aad50855 Human mu
41	37.8	92.2	1176	8	AAD50856	Aad50856 Human mod
42	37.8	92.2	1197	8	AAD50857	Aad50857 Human mod
43	37.8	92.2	1473	6	ABS54816	Abs54816 cDNA enco
44	37.8	92.2	1881	13	ADR44850	Adr44850 Porcine m
45	31.4	76.6	1149	6	ABX13057	Abx13057 Human MOR

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 81.4029 Seconds
                                            (without alignments)
                                            824.139 Million cell updates/sec

Title: US-09-883-839-1-386A_COPY_366_406
Perfect score: 41
Sequence: 1 ctgggcgggagagacagcct..........tgccctccgaccggcagtcc 41

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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                   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description
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     1   39.4   96.1   1182   4   US-09-826-509-546   Sequence 546, App
     2   39.4   96.1   1203   4   US-09-826-509-544   Sequence 544, App
     3   39.4   96.1   1610   3   US-08-889-108-7   Sequence 7, Appli
     4   39.4   96.1   1610   5   PCT-US94-10358-7   Sequence 7, Appli
     5   39.4   96.1   2160   3   US-08-188-275A-1   Sequence 1, Appli
     6   39.4   96.1   2162   3   US-09-351-198-1   Sequence 1, Appli
     7   39.4   96.1   2162   3   US-09-113-426-1   Sequence 1, Appli
     8   39.4   96.1   2162   4   US-09-016-434-1379   Sequence 1379, Ap
     9   39.4   96.1   2162   4   US-09-355-709C-7   Sequence 7, Appli
    10   31.4   76.6   1334   4   US-09-761-962A-3   Sequence 3, Appli
    11   31.4   76.6   1346   4   US-09-761-962A-12   Sequence 12, Appl
    12   31.4   76.6   1365   4   US-09-761-962A-11   Sequence 11, Appl

	13	31.4	76.6	1423	4	US-09-761-962A-1	Sequence 1, Appli
	14	31.4	76.6	1542	4	US-09-761-962A-4	Sequence 4, Appli
	15	31.4	76.6	1610	4	US-09-761-962A-16	Sequence 16, Appl
	16	31.4	76.6	1618	3	US-08-889-108-1	Sequence 1, Appli
	17	31.4	76.6	1618	3	US-08-889-108-3	Sequence 3, Appli
	18	31.4	76.6	1618	3	US-08-120-601B-1	Sequence 1, Appli
	19	31.4	76.6	1618	3	US-08-120-601B-3	Sequence 3, Appli
	20	31.4	76.6	1618	5	PCT-US94-10358-1	Sequence 1, Appli
	21	31.4	76.6	1618	5	PCT-US94-10358-3	Sequence 3, Appli
	22	31.4	76.6	1729	4	US-09-761-962A-9	Sequence 9, Appli
	23	31.4	76.6	1981	3	US-08-387-707-15	Sequence 15, Appl
	24	31.4	76.6	1981	3	US-08-405-271A-15	Sequence 15, Appl
	25	31.4	76.6	2045	4	US-09-761-962A-10	Sequence 10, Appl
	26	31.4	76.6	2135	3	US-08-430-286A-1	Sequence 1, Appli
	27	31.4	76.6	2229	4	US-09-214-904-1	Sequence 1, Appli
C	28	22.4	54.6	111	3	US-09-287-354-7	Sequence 7, Appli
C	29	22.4	54.6	111	3	US-09-287-354-8	Sequence 8, Appli
	30	21.8	53.2	601	4	US-09-949-016-137725	Sequence 137725,
	31	21.8	53.2	24707	4	US-09-740-027-3	Sequence 3, Appli
	32	21.8	53.2	24720	4	US-09-949-016-12341	Sequence 12341, A
	33	21.8	53.2	24721	4	US-09-949-016-15610	Sequence 15610, A
C	34	21.6	52.7	3247	3	US-09-221-017B-167	Sequence 167, App
C	35	20.6	50.2	36063	4	US-08-311-731A-140	Sequence 140, App
C	36	20.4	49.8	2214	4	US-09-902-540-9189	Sequence 9189, Ap
	37	20.4	49.8	9039	4	US-09-902-540-983	Sequence 983, App
C	38	20.4	49.8	145812	4	US-09-949-016-15698	Sequence 15698, A
	39	20.2	49.3	326	4	US-09-016-434-621	Sequence 621, App
C	40	20.2	49.3	747	4	US-09-252-991A-14123	Sequence 14123, A
C	41	20.2	49.3	1858	3	US-09-336-536-56	Sequence 56, Appl
	42	20.2	49.3	2085	4	US-09-252-991A-14016	Sequence 14016, A
	43	20.2	49.3	2115	4	US-09-252-991A-14060	Sequence 14060, A
	44	20.2	49.3	2130	4	US-09-489-039A-6065	Sequence 6065, Ap
C	45	20.2	49.3	2397	4	US-09-252-991A-14210	Sequence 14210, A

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:19 ; Search time 380.544 Seconds
                                          (without alignments)
                                          668.805 Million cell updates/sec

Title: US-09-883-839-1-386A_COPY.366_406
Perfect score: 41
Sequence: 1 ctgggcgggagagacagcct..........tgccctccgaccggcagtcc 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
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                 2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	39.4	96.1	178	16	US-10-029-386-14329	Sequence 14329, A
c	3	39.4	96.1	593	16	US-10-029-386-624	Sequence 624, App
	4	39.4	96.1	1182	10	US-09-826-509-546	Sequence 546, App
	5	39.4	96.1	1182	21	US-10-925-095-546	Sequence 546, App
	6	39.4	96.1	1203	10	US-09-826-509-544	Sequence 544, App
	7	39.4	96.1	1203	21	US-10-925-095-544	Sequence 544, App
	8	39.4	96.1	1239	14	US-10-080-917-10	Sequence 10, Appl
	9	39.4	96.1	1245	14	US-10-080-917-8	Sequence 8, Appli
	10	39.4	96.1	1388	14	US-10-185-083-26	Sequence 26, Appl
	11	39.4	96.1	1431	14	US-10-080-917-6	Sequence 6, Appli
	12	39.4	96.1	1464	14	US-10-185-083-25	Sequence 25, Appl
	13	39.4	96.1	2149	14	US-10-080-917-12	Sequence 12, Appl
	14	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	15	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	16	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	17	39.4	96.1	2162	11	US-09-883-839-7	Sequence 7, Appli
	18	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	19	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	20	39.4	96.1	2162	21	US-10-500-050-1	Sequence 1, Appli
	21	39.4	96.1	2279	21	US-10-477-714-33	Sequence 33, Appl
	22	37.8	92.2	1176	10	US-09-935-061-11	Sequence 11, Appl
	23	37.8	92.2	1176	10	US-09-935-061-13	Sequence 13, Appl
	24	37.8	92.2	1176	19	US-10-692-071-11	Sequence 11, Appl
	25	37.8	92.2	1176	19	US-10-692-071-13	Sequence 13, Appl
	26	37.8	92.2	1197	10	US-09-935-061-15	Sequence 15, Appl
	27	37.8	92.2	1197	19	US-10-692-071-15	Sequence 15, Appl
	28	37.8	92.2	1473	14	US-10-080-917-13	Sequence 13, Appl
	29	34.8	84.9	2165	11	US-09-883-839-9	Sequence 9, Appli
	30	31.4	76.6	1149	9	US-09-993-844-10	Sequence 10, Appl
	31	31.4	76.6	1149	23	US-11-026-435-10	Sequence 10, Appl
	32	31.4	76.6	1332	14	US-10-185-083-22	Sequence 22, Appl
	33	31.4	76.6	1334	9	US-09-761-962-3	Sequence 3, Appli
	34	31.4	76.6	1334	15	US-10-283-300-3	Sequence 3, Appli
	35	31.4	76.6	1346	9	US-09-761-962-12	Sequence 12, Appl
	36	31.4	76.6	1346	15	US-10-283-300-12	Sequence 12, Appl
	37	31.4	76.6	1365	9	US-09-761-962-11	Sequence 11, Appl
	38	31.4	76.6	1365	15	US-10-283-300-11	Sequence 11, Appl
	39	31.4	76.6	1373	14	US-10-185-083-51	Sequence 51, Appl
	40	31.4	76.6	1423	9	US-09-761-962-1	Sequence 1, Appli
	41	31.4	76.6	1423	15	US-10-283-300-1	Sequence 1, Appli
	42	31.4	76.6	1440	14	US-10-185-083-15	Sequence 15, Appl
	43	31.4	76.6	1542	9	US-09-761-962-4	Sequence 4, Appli
	44	31.4	76.6	1542	15	US-10-283-300-4	Sequence 4, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 2429.15 Seconds
                                          (without alignments)
                                          642.461 Million cell updates/sec

Title: US-09-883-839-1-386A_COPY_366_406
Perfect score: 41
Sequence: 1 ctgggcgggagagacagcct..........tgccctccgaccggcagtcc 41

Scoring table: IDENTITY_NUC
              ,   Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                   1: gb_est1:*
                   2: gb_est2:*
                   3: gb_htc:*
                   4: gb_est3:*
                   5: gb_est4:*
                   6: gb_est5:*
                   7: gb_est6:*
                   8: gb_gss1:*
                   9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
c   1   39.4   96.1   520   8   B82759   B82759 RPCI11-17K2
    2   39.4   96.1   582   5   BP346782   BP346782 BP346782
    3   39.4   96.1   750   7   CO934661   CO934661 AGENCOURT
c   4   38.4   93.7   245   8   AQ488720   AQ488720 RPCI-11-2
    5   37.8   92.2   718   7   CO928559   CO928559 AGENCOURT
c   6   31.4   76.6   525   8   AQ767579   AQ767579 HS_3206_A
    7   29.8   72.7   657   2   BB588668   BB588668 BB588668
    8   29.8   72.7   2405   3   AK038389   AK038389 Mus muscu
c   9   24   58.5   646   9   CE761270   CE761270 tigr-gss-

c	10	23.4	57.1	271	1	AV243802	AV243802	AV243802
c	11	23.4	57.1	368	2	BB802478	BB802478	BB802478
c	12	23.2	56.6	302	4	BI554683	BI554683	603236637
	13	23	56.1	653	2	BB642722	BB642722	BB642722
c	14	22.8	55.6	380	6	CB810557	CB810557	AMGNNUC:N
c	15	22.8	55.6	424	6	CB796826	CB796826	AMGNNUC:M
c	16	22.8	55.6	466	6	CB714860	CB714860	AMGNNUC:N
c	17	22.8	55.6	474	6	CB729592	CB729592	AMGNNUC:N
	18	22.6	55.1	408	5	BY238704	BY238704	BY238704
c	19	22.6	55.1	578	1	AV670617	AV670617	AV670617
c	20	22.4	54.6	326	5	BY360957	BY360957	BY360957
c	21	22.4	54.6	393	5	BY509437	BY509437	BY509437
c	22	22.4	54.6	540	7	CF948174	CF948174	UI-D-GC1-
c	23	22.4	54.6	815	7	CK194743	CK194743	FGAS00317
c	24	22.2	54.1	393	7	CN419044	CN419044	170004251
c	25	22.2	54.1	551	4	BI828568	BI828568	603078462
c	26	22.2	54.1	608	5	BX476106	BX476106	DKFZp686G
c	27	22.2	54.1	608	6	CA337453	CA337453	NISC_lw01
c	28	22.2	54.1	816	4	BG716163	BG716163	602677652
	29	22.2	54.1	945	9	CG304740	CG304740	OG5CT65TC
	30	22.2	54.1	987	8	CC421114	CC421114	PUHRN69TB
	31	22.2	54.1	1385	9	AG059978	AG059978	Pan trogl
	32	22	53.7	200	2	BF855386	BF855386	CM3-FN019
	33	22	53.7	406	4	BM862320	BM862320	mgcm002xB
c	34	22	53.7	535	7	CN669690	CN669690	A0883C06-
c	35	22	53.7	603	3	CNS08PUP	BX022925	Single re
c	36	22	53.7	610	1	AU050044	AU050044	AU050044
c	37	22	53.7	685	7	CF542110	CF542110	AGL357 An
c	38	22	53.7	704	3	CNS08RQZ	BX025383	Single re
c	39	22	53.7	707	3	CNS08ZCL	BX035233	Single re
c	40	22	53.7	714	4	BM609161	BM609161	170006870
c	41	22	53.7	749	5	BU237633	BU237633	603791078
	42	22	53.7	756	9	CG309639	CG309639	OGXEO27TV
c	43	22	53.7	769	9	CG309631	CG309631	OGXEO27TH
	44	22	53.7	788	9	CC632419	CC632419	OGLCF07TV
c	45	22	53.7	794	6	CB520280	CB520280	UI-M-GI0-

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 793.33 Seconds
                                         (without alignments)
                                         2504.208 Million cell updates/sec

Title: US-09-883-839-1-365T_COPY_345_385
Perfect score: 41
Sequence: 1 tgcggtccgaaccgcaccaa..........ctgggcgggagagacagcct 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   39.4   96.1   1182   6   AX280923   AX280923 Sequence
      2   39.4   96.1   1203   6   AX280921   AX280921 Sequence
      3   39.4   96.1   2160   6   AR162044   AR162044 Sequence
      4   39.4   96.1   2162   6   A87781   A87781 Sequence 7

	5	39.4	96.1	2162	6	AR181331	AR181331 Sequence
	6	39.4	96.1	2162	6	AR182295	AR182295 Sequence
	7	39.4	96.1	2162	6	AR270816	AR270816 Sequence
	8	39.4	96.1	2162	6	AR301230	AR301230 Sequence
	9	39.4	96.1	2162	6	AX548900	AX548900 Sequence
	10	39.4	96.1	2162	9	HUMMOR1X	L25119 Human Mu op
	11	37.8	92.2	305	9	HSOPRMI1	AF024515 Homo sapi
C	12	37.8	92.2	520	11	G53082	G53082 SHGC-84785
	13	37.8	92.2	1203	9	AF286024	AF286024 Macaca mu
	14	37.8	92.2	1203	9	AY521028	AY521028 Homo sapi
	15	37.8	92.2	1293	9	BC074927	BC074927 Homo sapi
	16	37.8	92.2	1388	9	AY036623	AY036623 Homo sapi
	17	37.8	92.2	1399	9	AY038989	AY038989 Macaca fa
	18	37.8	92.2	1464	9	AY036622	AY036622 Homo sapi
	19	37.8	92.2	1468	9	AY364230	AY364230 Homo sapi
	20	37.8	92.2	1473	9	HSU12569	U12569 Human mu op
	21	37.8	92.2	1610	6	AR106017	AR106017 Sequence
	22	37.8	92.2	1610	9	HUMOPIOIDA	L29301 Homo sapien
	23	37.8	92.2	2150	6	CQ725069	CQ725069 Sequence
	24	37.8	92.2	83889	9	AY587764	AY587764 Homo sapi
C	25	37.8	92.2	96310	9	AL136444	AL136444 Human DNA
	26	37.8	92.2	182048	2	AC027439	AC027439 Homo sapi
C	27	37.8	92.2	182383	2	AC021745	AC021745 Homo sapi
	28	34.6	84.4	1710	10	AY166606	AY166606 Cavia por
	29	33	80.5	1415	4	BTU89677	U89677 Bos taurus
	30	31.4	76.6	1881	4	AF521309	AF521309 Sus scrof
	31	31.4	76.6	1881	4	PIGMUOPR	L38645 Sus scrofa
	32	29.8	72.7	1367	10	RNU35424	U35424 Rattus norv
	33	29.8	72.7	1401	10	RATMOPIOID	L22455 Rat mu opio
	34	29.8	72.7	1448	10	RNU02083	U02083 Rattus norv
	35	29.8	72.7	1586	10	RATMORA	L13069 Rattus norv
	36	29.8	72.7	1618	6	AR106013	AR106013 Sequence
	37	29.8	72.7	1618	6	AR106014	AR106014 Sequence
	38	29.8	72.7	1618	6	AR153354	AR153354 Sequence
	39	29.8	72.7	1618	6	AR153355	AR153355 Sequence
	40	29.8	72.7	1944	10	S79903	S79903 mu opioid r
	41	29.8	72.7	2135	6	AR148257	AR148257 Sequence
	42	29.8	72.7	2135	10	RATMUOR1A	L20684 Rattus norv
	43	29.8	72.7	2397	10	RATRORB	D16349 Rattus norv
C	44	29.8	72.7	227058	2	AC115492	AC115492 Rattus no

Search completed: June 23, 2005, 01:02:30
Job time : 794.33 secs

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 279.437 Seconds
                                           (without alignments)
                                           868.566 Million cell updates/sec

Title: US-09-883-839-1-365T_COPY_345_385
Perfect score: 41
Sequence: 1 tgcggtccgaaccgcaccaa..........ctgggcgggagagacagcct 41

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
  No.   Score Match Length DB ID   Description
----
     1   39.4   96.1   1182 5 ABI98013   Abi98013 Non-endog
     2   39.4   96.1   1203 5 ABI98012   Abi98012 Non-endog

	3	39.4	96.1	2160	2	AAQ93102	Aaq93102 Human mu
	4	39.4	96.1	2162	2	AAV61995	Aav61995 Human mu-
	5	39.4	96.1	2162	2	AAV61986	Aav61986 Human mu-
	6	39.4	96.1	2162	2	AAV61991	Aav61991 Human mu-
	7	39.4	96.1	2162	2	AAV61988	Aav61988 Human mu-
	8	39.4	96.1	2162	2	AAV61984	Aav61984 Human mu-
	9	39.4	96.1	2162	2	AAV61994	Aav61994 Human mu-
	10	39.4	96.1	2162	2	AAV61987	Aav61987 Human mu-
	11	39.4	96.1	2162	2	AAV61992	Aav61992 Human mu-
	12	39.4	96.1	2162	2	AAV61990	Aav61990 Human mu-
	13	39.4	96.1	2162	2	AAV61993	Aav61993 Human mu-
	14	39.4	96.1	2162	2	AAV61985	Aav61985 Human mu-
	15	39.4	96.1	2162	2	AAV61989	Aav61989 Human mu-
	16	39.4	96.1	2162	3	AAZ88470	Aaz88470 Human mu
	17	39.4	96.1	2162	6	ABK14953	Abk14953 Human mu
	18	39.4	96.1	2162	8	ABZ42697	Abz42697 Human opi
	19	39.4	96.1	2162	10	ADC21534	Adc21534 Human DNA
	20	39.4	96.1	2162	10	ACA56781	Aca56781 Human sig
	21	39.4	96.1	2162	12	ADI56577	Adi56577 Human pol
	22	39.4	96.1	2162	12	ADO30013	Ado30013 Human GPC
c	23	37.8	92.2	178	12	ACH81134	Ach81134 Human gen
c	24	37.8	92.2	593	12	ACH67429	Ach67429 Human gen
	25	37.8	92.2	1176	8	AAD50855	Aad50855 Human mu
	26	37.8	92.2	1176	8	AAD50856	Aad50856 Human mod
	27	37.8	92.2	1197	8	AAD50857	Aad50857 Human mod
	28	37.8	92.2	1200	13	ADR44830	Adr44830 Human HUM
	29	37.8	92.2	1200	13	ADR44837	Adr44837 HUMOR mut
	30	37.8	92.2	1239	6	ABS54814	Abs54814 cDNA enco
	31	37.8	92.2	1245	6	ABS54813	Abs54813 cDNA enco
	32	37.8	92.2	1388	10	ADG42251	Adg42251 Mu-opioid
	33	37.8	92.2	1431	6	ABS54812	Abs54812 cDNA enco
	34	37.8	92.2	1464	10	ADG42250	Adg42250 Mu-opioid
	35	37.8	92.2	1473	6	ABS54816	Abs54816 cDNA enco
	36	37.8	92.2	1610	2	AAQ89226	Aaq89226 Human mu
	37	37.8	92.2	1610	3	AAA59503	Aaa59503 cDNA enco
	38	37.8	92.2	1610	13	ADR44881	Adr44881 Human mu-
	39	37.8	92.2	2149	6	ABS54815	Abs54815 cDNA enco
	40	37.8	92.2	2279	8	AAD51226	Aad51226 Human REM
	41	37.8	92.2	9426	13	ADR44835	Adr44835 FIV opioi
c	42	37.8	92.2	9569	13	ADR44842	Adr44842 FIV-NSE-H
	43	37.8	92.2	10472	13	ADR44876	Adr44876 Plasmid p
	44	33	80.5	1415	13	ADR44844	Adr44844 Bovine mu
	45	31.4	76.6	1881	13	ADR44850	Adr44850 Porcine m

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 81.4029 Seconds
                                            (without alignments)
                                            824.139 Million cell updates/sec

Title: US-09-883-839-1-365T_COPY_345_385
Perfect score: 41
Sequence: 1 tgcggtccgaaccgcaccaa..........ctgggcgggagagacagcct 41

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39.4	96.1	1182	4	US-09-826-509-546	Sequence 546, App
2	39.4	96.1	1203	4	US-09-826-509-544	Sequence 544, App
3	39.4	96.1	2160	3	US-08-188-275A-1	Sequence 1, Appli
4	39.4	96.1	2162	3	US-09-351-198-1	Sequence 1, Appli
5	39.4	96.1	2162	3	US-09-113-426-1	Sequence 1, Appli
6	39.4	96.1	2162	4	US-09-016-434-1379	Sequence 1379, Ap
7	39.4	96.1	2162	4	US-09-355-709C-7	Sequence 7, Appli
8	37.8	92.2	1610	3	US-08-889-108-7	Sequence 7, Appli
9	37.8	92.2	1610	5	PCT-US94-10358-7	Sequence 7, Appli
10	29.8	72.7	1618	3	US-08-889-108-1	Sequence 1, Appli
11	29.8	72.7	1618	3	US-08-889-108-3	Sequence 3, Appli
12	29.8	72.7	1618	3	US-08-120-601B-1	Sequence 1, Appli

	13	29.8	72.7	1618	3	US-08-120-601B-3	Sequence 3, Appli
	14	29.8	72.7	1618	5	PCT-US94-10358-1	Sequence 1, Appli
	15	29.8	72.7	1618	5	PCT-US94-10358-3	Sequence 3, Appli
	16	29.8	72.7	2135	3	US-08-430-286A-1	Sequence 1, Appli
	17	28.2	68.8	1334	4	US-09-761-962A-3	Sequence 3, Appli
	18	28.2	68.8	1346	4	US-09-761-962A-12	Sequence 12, Appl
	19	28.2	68.8	1365	4	US-09-761-962A-11	Sequence 11, Appl
	20	28.2	68.8	1423	4	US-09-761-962A-1	Sequence 1, Appli
	21	28.2	68.8	1542	4	US-09-761-962A-4	Sequence 4, Appli
	22	28.2	68.8	1610	4	US-09-761-962A-16	Sequence 16, Appl
	23	28.2	68.8	1729	4	US-09-761-962A-9	Sequence 9, Appli
	24	28.2	68.8	2045	4	US-09-761-962A-10	Sequence 10, Appl
	25	28.2	68.8	2229	4	US-09-214-904-1	Sequence 1, Appli
	26	25	61.0	1981	3	US-08-387-707-15	Sequence 15, Appl
	27	25	61.0	1981	3	US-08-405-271A-15	Sequence 15, Appl
	28	22	53.7	601	4	US-09-949-016-28616	Sequence 28616, A
	29	22	53.7	601	4	US-09-949-016-28617	Sequence 28617, A
	30	22	53.7	601	4	US-09-949-016-28618	Sequence 28618, A
	31	22	53.7	601	4	US-09-949-016-28619	Sequence 28619, A
	32	22	53.7	601	4	US-09-949-016-170547	Sequence 170547,
	33	22	53.7	601	4	US-09-949-016-170548	Sequence 170548,
	34	22	53.7	601	4	US-09-949-016-170549	Sequence 170549,
	35	22	53.7	601	4	US-09-949-016-170550	Sequence 170550,
c	36	22	53.7	67156	4	US-09-949-016-12284	Sequence 12284, A
c	37	22	53.7	67157	4	US-09-949-016-16558	Sequence 16558, A
	38	21.4	52.2	1378	2	US-08-776-585-2	Sequence 2, Appli
	39	21.4	52.2	1400	2	US-08-776-585-1	Sequence 1, Appli
c	40	20.8	50.7	325	3	US-09-439-313-391	Sequence 391, App
c	41	20.8	50.7	325	3	US-09-352-616A-391	Sequence 391, App
c	42	20.8	50.7	325	4	US-09-636-215-391	Sequence 391, App
c	43	20.8	50.7	325	4	US-09-685-166A-391	Sequence 391, App
c	44	20.8	50.7	325	4	US-09-679-426-391	Sequence 391, App
c	45	20.8	50.7	325	4	US-09-759-143-391	Sequence 391, App

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:19 ; Search time 380.544 Seconds
                                           (without alignments)
                                           668.805 Million cell updates/sec

Title: US-09-883-839-1-365T_COPY_345_385
Perfect score: 41
Sequence: 1 tgcggtccgaaccgcaccaa.........ctgggcgggagagacagcct 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
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                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	41	100.0	2162	11	US-09-883-839-7	Sequence 7, Appli
	2	39.4	96.1	1182	10	US-09-826-509-546	Sequence 546, App
	3	39.4	96.1	1182	21	US-10-925-095-546	Sequence 546, App
	4	39.4	96.1	1203	10	US-09-826-509-544	Sequence 544, App
	5	39.4	96.1	1203	21	US-10-925-095-544	Sequence 544, App
	6	39.4	96.1	2162	11	US-09-883-839-1	Sequence 1, Appli
	7	39.4	96.1	2162	11	US-09-883-839-3	Sequence 3, Appli
	8	39.4	96.1	2162	11	US-09-883-839-5	Sequence 5, Appli
	9	39.4	96.1	2162	11	US-09-883-839-8	Sequence 8, Appli
	10	39.4	96.1	2162	15	US-10-225-567A-185	Sequence 185, App
	11	39.4	96.1	2162	17	US-10-305-720-1379	Sequence 1379, Ap
	12	39.4	96.1	2162	21	US-10-500-050-1	Sequence 1, Appli
	13	39.4	96.1	2165	11	US-09-883-839-9	Sequence 9, Appli
C	14	37.8	92.2	178	16	US-10-029-386-14329	Sequence 14329, A
C	15	37.8	92.2	593	16	US-10-029-386-624	Sequence 624, App
	16	37.8	92.2	1176	10	US-09-935-061-11	Sequence 11, Appl
	17	37.8	92.2	1176	10	US-09-935-061-13	Sequence 13, Appl
	18	37.8	92.2	1176	19	US-10-692-071-11	Sequence 11, Appl
	19	37.8	92.2	1176	19	US-10-692-071-13	Sequence 13, Appl
	20	37.8	92.2	1197	10	US-09-935-061-15	Sequence 15, Appl
	21	37.8	92.2	1197	19	US-10-692-071-15	Sequence 15, Appl
	22	37.8	92.2	1239	14	US-10-080-917-10	Sequence 10, Appl
	23	37.8	92.2	1245	14	US-10-080-917-8	Sequence 8, Appli
	24	37.8	92.2	1388	14	US-10-185-083-26	Sequence 26, Appl
	25	37.8	92.2	1431	14	US-10-080-917-6	Sequence 6, Appli
	26	37.8	92.2	1464	14	US-10-185-083-25	Sequence 25, Appl
	27	37.8	92.2	1473	14	US-10-080-917-13	Sequence 13, Appl
	28	37.8	92.2	2149	14	US-10-080-917-12	Sequence 12, Appl
	29	37.8	92.2	2279	21	US-10-477-714-33	Sequence 33, Appl
	30	29.8	72.7	1149	9	US-09-993-844-10	Sequence 10, Appl
	31	29.8	72.7	1149	23	US-11-026-435-10	Sequence 10, Appl
	32	29.8	72.7	1618	10	US-09-841-720-1	Sequence 1, Appli
	33	29.8	72.7	1618	10	US-09-841-720-3	Sequence 3, Appli
	34	28.2	68.8	1332	14	US-10-185-083-22	Sequence 22, Appl
	35	28.2	68.8	1334	9	US-09-761-962-3	Sequence 3, Appli
	36	28.2	68.8	1334	15	US-10-283-300-3	Sequence 3, Appli
	37	28.2	68.8	1346	9	US-09-761-962-12	Sequence 12, Appl
	38	28.2	68.8	1346	15	US-10-283-300-12	Sequence 12, Appl
	39	28.2	68.8	1365	9	US-09-761-962-11	Sequence 11, Appl
	40	28.2	68.8	1365	15	US-10-283-300-11	Sequence 11, Appl
	41	28.2	68.8	1373	14	US-10-185-083-51	Sequence 51, Appl
	42	28.2	68.8	1423	9	US-09-761-962-1	Sequence 1, Appli
	43	28.2	68.8	1423	15	US-10-283-300-1	Sequence 1, Appli
	44	28.2	68.8	1440	14	US-10-185-083-15	Sequence 15, Appl
	45	28.2	68.8	1542	9	US-09-761-962-4	Sequence 4, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 11:48:18 ; Search time 2429.15 Seconds
                                          (without alignments)
                                          642.461 Million cell updates/sec

Title: US-09-883-839-1-365T_COPY_345_385
Perfect score: 41
Sequence: 1 tgcggtccgaaccgcaccaa..........ctgggcgggagagacagcct 41

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                               SUMMARIES
                         %
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      3   37.8   92.2   750   7   CO934661   CO934661 AGENCOURT
      4   36.2   88.3   718   7   CO928559   CO928559 AGENCOURT
  c   5   29.8   72.7   525   8   AQ767579   AQ767579 HS_3206_A
      6   28.2   68.8   657   2   BB588668   BB588668 BB588668
      7   28.2   68.8   2405   3   AK038389   AK038389 Mus muscu
  c   8   24   58.5   624   1   AV745148   AV745148 AV745148
  c   9   23.4   57.1   329   1   AA313872   AA313872 EST185729

C	10	23.4	57.1	334	1	AA093521	AA093521 c10075.se
C	11	23.4	57.1	366	2	AW352266	AW352266 CM2-HT013
C	12	23.4	57.1	418	7	T68202	T68202 yc40a05.r1
C	13	23.4	57.1	430	2	AW389789	AW389789 RC2-ST017
C	14	23.4	57.1	442	2	AW389846	AW389846 RC2-ST017
C	15	23.4	57.1	469	7	CF139013	CF139013 UI-HF-CB0
C	16	23.4	57.1	587	1	AA459583	AA459583 aa27g02.r
C	17	23.4	57.1	624	2	AW958372	AW958372 EST370442
C	18	23.4	57.1	684	7	CN297906	CN297906 170005316
C	19	23.4	57.1	691	4	BG338370	BG338370 602436153
C	20	23.4	57.1	738	2	BE390804	BE390804 601286511
C	21	23.4	57.1	774	4	BI829052	BI829052 603079142
C	22	23.4	57.1	809	4	BG744023	BG744023 602722802
C	23	23.4	57.1	810	6	CD580268	CD580268 EST_PSF01
C	24	23.4	57.1	817	1	AL524403	AL524403 AL524403
C	25	23.4	57.1	834	4	BI858369	BI858369 603383954
C	26	23.4	57.1	864	5	BQ941562	BQ941562 AGENCOURT
C	27	23.4	57.1	875	1	AU122630	AU122630 AU122630
C	28	23.4	57.1	877	2	BF529446	BF529446 602041986
C	29	23.4	57.1	880	5	BU156291	BU156291 AGENCOURT
C	30	23.4	57.1	891	5	BQ441924	BQ441924 AGENCOURT
C	31	23.4	57.1	909	5	BU902610	BU902610 AGENCOURT
C	32	23.4	57.1	911	1	AL537676	AL537676 AL537676
C	33	23.4	57.1	915	5	BQ652037	BQ652037 AGENCOURT
C	34	23.4	57.1	918	5	BQ669711	BQ669711 AGENCOURT
C	35	23.4	57.1	921	5	BQ645892	BQ645892 AGENCOURT
C	36	23.4	57.1	938	5	BU845541	BU845541 AGENCOURT
C	37	23.4	57.1	940	1	AL574285	AL574285 AL574285
C	38	23.4	57.1	975	5	BQ060734	BQ060734 AGENCOURT
C	39	23.4	57.1	978	5	BQ051523	BQ051523 AGENCOURT
C	40	23.4	57.1	987	5	BQ055835	BQ055835 AGENCOURT
C	41	23.4	57.1	990	4	BI115686	BI115686 602866031
C	42	23.4	57.1	991	5	BQ064595	BQ064595 AGENCOURT
C	43	23.4	57.1	1061	4	BM468448	BM468448 AGENCOURT
C	44	23.4	57.1	1140	4	BM455223	BM455223 AGENCOURT
C	45	23.4	57.1	1153	4	BM564265	BM564265 AGENCOURT

From:	Switzer, Juliet
Sent:	Wednesday, May 04, 2005 3:33 PM
To:	STIC-Biotech/ChemLib
Subject:	please search

for US 09/883839 please search

in all GenEmbl, GenSeq, USPATS issued, PGPUBS, and EST databases
1. Seq ID NO 1 from nucleotide 47-87 where the nucleotide at postition 67 is a "C"
2. Seq ID NO 1 from nucleotide 104-144 where the nucleotide at postition 124 is a "A"
3. Seq ID NO 1 from nucleotide 133-173 where the nucleotide at postition 153 is a "T"
4. Seq ID NO 1 from nucleotide 154-194 where the nucleotide at postition 174 is a "A"
5. Seq ID NO 1 from nucleotide167-207 where there is an insertion of "GGC"
immediately after nucleotide position 187.

Please search in ALL PRIOR ART amino acid databases
6. SEQ ID NO 2 from aa 15-30 where teh aa at postion 23 is PRO
7. SEQ ID NO 2 from aa 35-55 where teh aa at postion 42 is THR
8. SEQ ID NO 2 from aa 55-70 where there is GLY inserted after GLY 63.

PLEASE RETURN RESULTS ON DISK.
THanks.

Juliet Switzer
Art Unit 1634
phone: 571-272-753
office: Remsen 2A61

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OM protein - protein search, using sw model

Run on: May 12, 2005, 10:01:03 ; Search time 90.566 Seconds
                                       (without alignments)
                                       68.328 Million cell updates/sec

Title: US-09-883-839-2-INS-GLY_COPY_55_70
Perfect score: 88
Sequence: 1 RDSLCPPTGgSPSMIT 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                         %
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     3   71.5   81.2   392   6   AAE33275   Aae33275 Human mu
     4   71.5   81.2   399   6   AAE33277   Aae33277 Human mod
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     6   71.5   81.2   400   2   AAR76780   Aar76780 Human mu
     7   71.5   81.2   400   3   AAY79946   Aay79946 Human mu
     8   71.5   81.2   400   3   AAY79949   Aay79949 Human mu
     9   71.5   81.2   400   3   AAY79945   Aay79945 Human mu

10	71.5	81.2	400	3	AAY79948	Aay79948 Human mu
11	71.5	81.2	400	3	AAY79947	Aay79947 Human mu
12	71.5	81.2	400	3	AAB07866	Aab07866 A human m
13	71.5	81.2	400	4	ABB56376	Abb56376 Non-endog
14	71.5	81.2	400	5	AAU76034	Aau76034 Human mu
15	71.5	81.2	400	6	ABP81851	Abp81851 Human opi
16	71.5	81.2	400	8	ADH50093	Adh50093 Human mu
17	71.5	81.2	400	8	ADH50086	Adh50086 Human mu
18	71.5	81.2	400	8	ADO29588	Ado29588 Human GPC
19	71.5	81.2	400	8	ADN38673	Adn38673 Wild type
20	71.5	81.2	400	8	ADR44838	Adr44838 HUMOR mut
21	71.5	81.2	400	8	ADR44829	Adr44829 Human HUM
22	71.5	81.2	412	5	ABG32261	Abg32261 Human mu2
23	71.5	81.2	414	5	ABG32260	Abg32260 Human mu2
24	71.5	81.2	415	5	ABG33032	Abg33032 Human mu
25	71.5	81.2	418	7	ADG42210	Adg42210 Mu-opioid
26	71.5	81.2	446	7	ADG42209	Adg42209 Mu-opioid
27	71.5	81.2	462	6	AAE33476	Aae33476 Human REM
28	71.5	81.2	476	5	ABG32259	Abg32259 Human mu1
29	65.5	74.4	400	8	ADH50094	Adh50094 Pig mu op
30	65.5	74.4	401	8	ADR44849	Adr44849 Porcine m
31	57.5	65.3	356	2	AAR65188	Aar65188 Murine mu
32	57.5	65.3	356	4	AAB68440	Aab68440 Amino aci
33	57.5	65.3	382	5	ABG75675	Abg75675 Human MOR
34	57.5	65.3	382	8	ADO28783	Ado28783 Arrestin
35	57.5	65.3	398	2	AAR71964	Aar71964 Rat mu op
36	57.5	65.3	398	2	AAR76781	Aar76781 Rat mu op
37	57.5	65.3	398	3	AAY80494	Aay80494 Rat mu-op
38	57.5	65.3	398	3	AAB07864	Aab07864 Amino aci
39	57.5	65.3	398	5	AAU96238	Aau96238 Rat mu op
40	57.5	65.3	398	5	ABG32797	Abg32797 Rat mu op
41	57.5	65.3	398	5	ABG32798	Abg32798 Rat mu op
42	57.5	65.3	398	8	ADH50009	Adh50009 Wild-type
43	57.5	65.3	398	8	ADH50087	Adh50087 Rat mu op
44	57.5	65.3	398	8	ADH50096	Adh50096 Mutant ra
45	57.5	65.3	398	8	ADN38675	Adn38675 Wild type

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OM protein - protein search, using sw model

Run on: May 12, 2005, 10:06:54 ; Search time 23.2453 Seconds
                                         (without alignments)
                                         51.382 Million cell updates/sec

Title: US-09-883-839-2-INS-GLY_COPY_55_70
Perfect score: 88
Sequence: 1 RDSLCPPTGgSPSMIT 16

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

                    %
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   No.   Score Match Length DB ID   Description
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      2   71.5   81.2   400 3 US-08-889-108-8   Sequence 8, Appli
      3   71.5   81.2   400 3 US-08-188-275A-2   Sequence 2, Appli
      4   71.5   81.2   400 3 US-09-351-198-2   Sequence 2, Appli
      5   71.5   81.2   400 3 US-09-113-426-2   Sequence 2, Appli
      6   71.5   81.2   400 4 US-09-826-509-545   Sequence 545, App
      7   71.5   81.2   400 5 PCT-US94-10358-8   Sequence 8, Appli
      8   71.5   81.2   415 4 US-08-405-271A-20   Sequence 20, Appl
      9   57.5   65.3   356 3 US-08-430-286A-2   Sequence 2, Appli
     10   57.5   65.3   356 3 US-08-430-286A-5   Sequence 5, Appli
     11   57.5   65.3   391 2 US-08-454-549-3   Sequence 3, Appli
     12   57.5   65.3   391 3 US-08-454-552-3   Sequence 3, Appli

13	57.5	65.3	391	3	US-08-676-351-4	Sequence 4, Appli
14	57.5	65.3	398	1	US-08-149-093A-5	Sequence 5, Appli
15	57.5	65.3	398	2	US-08-911-245-5	Sequence 5, Appli
16	57.5	65.3	398	2	US-08-514-451A-8	Sequence 8, Appli
17	57.5	65.3	398	3	US-09-170-331-5	Sequence 5, Appli
18	57.5	65.3	398	3	US-08-889-108-2	Sequence 2, Appli
19	57.5	65.3	398	3	US-08-120-601B-2	Sequence 2, Appli
20	57.5	65.3	398	3	US-08-188-275A-3	Sequence 3, Appli
21	57.5	65.3	398	3	US-08-387-707-16	Sequence 16, Appl
22	57.5	65.3	398	3	US-09-510-473-5	Sequence 5, Appli
23	57.5	65.3	398	3	US-09-351-198-3	Sequence 3, Appli
24	57.5	65.3	398	3	US-09-113-426-3	Sequence 3, Appli
25	57.5	65.3	398	4	US-09-048-916B-7	Sequence 7, Appli
26	57.5	65.3	398	4	US-08-405-271A-16	Sequence 16, Appl
27	57.5	65.3	398	5	PCT-US94-10358-2	Sequence 2, Appli
28	51.5	58.5	390	4	US-09-761-962A-25	Sequence 25, Appl
29	51.5	58.5	391	4	US-09-761-962A-26	Sequence 26, Appl
30	51.5	58.5	392	4	US-09-761-962A-19	Sequence 19, Appl
31	51.5	58.5	398	4	US-09-761-962A-29	Sequence 29, Appl
32	51.5	58.5	398	4	US-09-214-904-2	Sequence 2, Appli
33	51.5	58.5	401	4	US-09-761-962A-20	Sequence 20, Appl
34	51.5	58.5	409	4	US-09-761-962A-27	Sequence 27, Appl
35	51.5	58.5	438	4	US-09-761-962A-17	Sequence 17, Appl
36	51.5	58.5	444	4	US-09-761-962A-28	Sequence 28, Appl
37	49	55.7	230	4	US-09-270-767-35198	Sequence 35198, A
38	49	55.7	230	4	US-09-270-767-50415	Sequence 50415, A
39	48	54.5	89	4	US-08-793-273C-9	Sequence 9, Appli
40	48	54.5	89	5	PCT-US95-11684-9	Sequence 9, Appli
41	48	54.5	98	4	US-09-252-991A-31130	Sequence 31130, A
42	47	53.4	89	4	US-08-793-273C-8	Sequence 8, Appli
43	47	53.4	89	5	PCT-US95-11684-8	Sequence 8, Appli
44	47	53.4	2199	4	US-08-793-273C-2	Sequence 2, Appli
45	47	53.4	2199	5	PCT-US95-11684-2	Sequence 2, Appli

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2005, 10:09:59 ; Search time 69.7358 Seconds
                                        (without alignments)
                                        76.644 Million cell updates/sec

Title: US-09-883-839-2-INS-GLY_COPY_55_70
Perfect score: 88
Sequence: 1 RDSLCPPTGgSPSMIT 16

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
              1:   /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
              2:   /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
              3:   /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
              4:   /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
              5:   /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
              6:   /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
              7:   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
              8:   /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
              9:   /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
             10:   /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
             11:   /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
             12:   /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
             13:   /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
             14:   /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
             15:   /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
             16:   /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
             17:   /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
             18:   /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
             19:   /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
             20:   /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                        %
Result   Query

No.	Score	Match	Length	DB	ID	Description
1	88	100.0	401	11	US-09-883-839-10	Sequence 10, Appl
2	71.5	81.2	392	10	US-09-935-061-12	Sequence 12, Appl
3	71.5	81.2	392	10	US-09-935-061-14	Sequence 14, Appl
4	71.5	81.2	392	10	US-09-826-509-547	Sequence 547, App
5	71.5	81.2	392	16	US-10-692-071-12	Sequence 12, Appl
6	71.5	81.2	392	16	US-10-692-071-14	Sequence 14, Appl
7	71.5	81.2	392	17	US-10-925-095-547	Sequence 547, App
8	71.5	81.2	399	10	US-09-935-061-16	Sequence 16, Appl
9	71.5	81.2	399	16	US-10-692-071-16	Sequence 16, Appl
10	71.5	81.2	400	9	US-09-966-871-78	Sequence 78, Appl
11	71.5	81.2	400	9	US-09-966-871-85	Sequence 85, Appl
12	71.5	81.2	400	10	US-09-826-509-545	Sequence 545, App
13	71.5	81.2	400	11	US-09-883-839-2	Sequence 2, Appli
14	71.5	81.2	400	11	US-09-883-839-4	Sequence 4, Appli
15	71.5	81.2	400	11	US-09-883-839-6	Sequence 6, Appli
16	71.5	81.2	400	13	US-10-039-645-78	Sequence 78, Appl
17	71.5	81.2	400	13	US-10-039-645-85	Sequence 85, Appl
18	71.5	81.2	400	14	US-10-225-567A-186	Sequence 186, App
19	71.5	81.2	400	15	US-10-458-860-78	Sequence 78, Appl
20	71.5	81.2	400	15	US-10-458-860-85	Sequence 85, Appl
21	71.5	81.2	400	15	US-10-465-172A-7	Sequence 7, Appli
22	71.5	81.2	400	17	US-10-925-095-545	Sequence 545, App
23	71.5	81.2	412	14	US-10-080-917-11	Sequence 11, Appl
24	71.5	81.2	414	14	US-10-080-917-9	Sequence 9, Appli
25	71.5	81.2	415	9	US-09-823-114-20	Sequence 20, Appl
26	71.5	81.2	415	14	US-10-290-748-20	Sequence 20, Appl
27	71.5	81.2	418	14	US-10-185-083-40	Sequence 40, Appl
28	71.5	81.2	446	14	US-10-185-083-39	Sequence 39, Appl
29	71.5	81.2	462	17	US-10-477-714-7	Sequence 7, Appli
30	71.5	81.2	476	14	US-10-080-917-7	Sequence 7, Appli
31	65.5	74.4	400	9	US-09-966-871-86	Sequence 86, Appl
32	65.5	74.4	400	13	US-10-039-645-86	Sequence 86, Appl
33	65.5	74.4	400	15	US-10-458-860-86	Sequence 86, Appl
34	57.5	65.3	382	9	US-09-993-844-4	Sequence 4, Appli
35	57.5	65.3	382	15	US-10-633-438-61	Sequence 61, Appl
36	57.5	65.3	398	9	US-09-823-114-16	Sequence 16, Appl
37	57.5	65.3	398	9	US-09-966-871-1	Sequence 1, Appli
38	57.5	65.3	398	9	US-09-966-871-79	Sequence 79, Appl
39	57.5	65.3	398	10	US-09-841-720-2	Sequence 2, Appli
40	57.5	65.3	398	13	US-10-039-645-1	Sequence 1, Appli
41	57.5	65.3	398	13	US-10-039-645-79	Sequence 79, Appl
42	57.5	65.3	398	14	US-10-290-748-16	Sequence 16, Appl
43	57.5	65.3	398	15	US-10-458-860-1	Sequence 1, Appli
44	57.5	65.3	398	15	US-10-458-860-79	Sequence 79, Appl

Run on: May 12, 2005, 10:05:49 ; Search time 17.2075 Seconds
                                           (without alignments)
                                           89.465 Million cell updates/sec

Title: US-09-883-839-2-INS-GLY_COPY_55_70
Perfect score: 88
Sequence: 1 RDSLCPPTGgSPSMIT 16

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                   1: pir1:*
                   2: pir2:*
                   3: pir3:*
                   4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
  No.   Score Match Length DB   ID   Description
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     1   71.5   81.2   392 2   S65693   opioid receptor mu
     2   71.5   81.2   400 2   I56553   mu opiate receptor
     3   57.5   65.3   398 2   I56517   mu opioid receptor
     4   57.5   65.3   398 2   I56504   mu opioid receptor
     5   51.5   58.5   398 2   A57510   mu opioid receptor
     6   48   54.5   1403 2   S24548   homeotic protein p
     7   48   54.5   2019 1   JQ1322   tenascin precursor
     8   47   53.4   229 2   T31190   hypothetical prote
     9   47   53.4   2201 2   A32160   tenascin-C - human
    10   46   52.3   575 2   A54861   tenascin - rat (fr
    11   46   52.3   772 2   T43034   kinesin-like prote
    12   46   52.3   775 2   T43033   kinesin-like prote
    13   45   51.1   789 2   A39564   transcription repr
    14   44.5   50.6   442 2   H69181   hypothetical prote
    15   44   50.0   389 2   AC2268   heterocyst envelop
    16   44   50.0   461 2   T35151   hypothetical prote
    17   44   50.0   648 2   T23864   hypothetical prote
    18   43   48.9   563 2   JQ0623   nerve growth facto
    19   43   48.9   598 2   A37251   probable nuclear h
    20   43   48.9   601 1   QRMSN1   probable hormone r

21	43	48.9	859	2	T35785	probable beta-gluc
22	43	48.9	885	2	G83260	aminopeptidase N P
23	43	48.9	1746	1	S19694	tenascin precursor
24	43	48.9	1810	1	A32230	tenascin precursor
25	42	47.7	222	2	D95307	hypothetical prote
26	42	47.7	302	2	D36786	hypothetical prote
27	42	47.7	465	2	G02738	FREAC-4 - human
28	42	47.7	1375	2	T18961	FAB1 protein homol
29	41	46.6	199	2	T52410	blue copper-bindin
30	41	46.6	201	2	T52408	blue copper-bindin
31	41	46.6	202	2	T01605	phytocyanin At2g44
32	41	46.6	293	2	AC2780	tolB protein [impo
33	41	46.6	293	2	E97559	tolb protein precu
34	41	46.6	409	2	AI1857	tryptophan synthas
35	41	46.6	705	2	T22201	hypothetical prote
36	41	46.6	806	1	TVHUF3	fibroblast growth
37	41	46.6	933	2	A31930	cytotactin - chick
38	41	46.6	948	2	A57640	retinoblastoma bin
39	41	46.6	1145	2	T05573	hypothetical prote
40	41	46.6	1207	2	T00378	KIAA0641 protein -
41	40.5	46.0	1003	2	A38234	oxoglutarate dehyd
42	40	45.5	76	2	T09262	glycine-rich cell
43	40	45.5	318	2	T49714	related to spliceo
44	40	45.5	336	2	AG0307	conserved hypothet
45	40	45.5	357	2	T02443	probable peroxidas

Run on: May 12, 2005, 10:04:59 ; Search time 83.9245 Seconds
                                             (without alignments)
                                             97.627 Million cell updates/sec

Title: US-09-883-839-2-INS-GLY_COPY_55_70
Perfect score: 88
Sequence: 1 RDSLCPPTGgSPSMIT 16

Scoring table: BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                     1: uniprot_sprot:*
                     2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score Match Length DB ID   Description
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     1   71.5   81.2   89   2 O43185   O43185 homo sapien
     2   71.5   81.2   400   1 OPRM_HUMAN   P35372 homo sapien
     3   71.5   81.2   400   1 OPRM_MACMU   Q9myw9 macaca mula
     4   71.5   81.2   400   2 Q95M54   Q95m54 macaca fasc
     5   71.5   81.2   402   2 Q6UQ80   Q6uq80 homo sapien
     6   71.5   81.2   418   2 Q8IWW3   Q8iww3 homo sapien
     7   71.5   81.2   446   2 Q8IWW4   Q8iww4 homo sapien
     8   71.5   81.2   454   2 Q9H573   Q9h573 homo sapien
     9   66.5   75.6   400   2 Q8CGM4   Q8cgm4 cavia porce
    10   65.5   74.4   401   1 OPRM_PIG   Q95247 sus scrofa
    11   57.5   65.3   94   2 Q80WZ4   Q80wz4 rattus sp.
    12   57.5   65.3   398   1 OPRM_RAT   P33535 rattus norv
    13   51.5   58.5   70   2 Q71UR0   Q71ur0 mus musculu
    14   51.5   58.5   388   2 Q8CH75   Q8ch75 mus musculu
    15   51.5   58.5   390   2 Q8VI71   Q8vi71 mus musculu
    16   51.5   58.5   391   2 Q8VI70   Q8vi70 mus musculu
    17   51.5   58.5   392   2 Q8CH74   Q8ch74 mus musculu
    18   51.5   58.5   393   2 Q9R1M0   Q9r1m0 mus musculu
    19   51.5   58.5   398   1 OPRM_MOUSE   P42866 mus musculu
    20   51.5   58.5   401   2 Q9R1L9   Q9r1l9 mus musculu
    21   51.5   58.5   409   2 Q8VI69   Q8vi69 mus musculu
    22   51.5   58.5   416   2 Q6YC50   Q6yc50 mus musculu

23	51.5	58.5	425	2	Q8CH73	Q8ch73	mus musculu
24	51.5	58.5	438	2	Q9R0D1	Q9r0d1	mus musculu
25	51.5	58.5	444	2	Q9JIY1	Q9jiy1	mus musculu
26	51.5	58.5	456	2	Q8CGW2	Q8cgw2	mus musculu
27	50.5	57.4	401	1	OPRM_BOVIN	P79350	bos taurus
28	49	55.7	644	2	Q9VJ57	Q9vj57	drosophila
29	49	55.7	646	2	Q86LC4	Q86lc4	drosophila
30	48	54.5	1403	1	PROS_DROME	P29617	drosophila
31	48	54.5	2019	2	Q64706	Q64706	mus musculu
32	48	54.5	2019	2	Q80YX2	Q80yx2	mus musculu
33	48	54.5	2110	2	Q80YX1	Q80yx1	mus musculu
34	47	53.4	229	2	O85899	O85899	sphingomona
35	47	53.4	588	2	Q6D1K4	Q6d1k4	erwinia car
36	47	53.4	2201	1	TENA_HUMAN	P24821	homo sapien
37	46.5	52.8	186	2	Q6ERG2	Q6erg2	oryza sativ
38	46.5	52.8	610	2	Q9U450	Q9u450	drosophila
39	46.5	52.8	621	2	Q8MRI9	Q8mri9	drosophila
40	46.5	52.8	698	2	Q9VGZ5	Q9vgz5	drosophila
41	46.5	52.8	2030	2	Q9VXV3	Q9vxv3	drosophila
42	46	52.3	120	2	Q62659	Q62659	rattus norv
43	46	52.3	211	2	Q62660	Q62660	rattus norv
44	46	52.3	346	1	PER9_ARATH	Q96512	arabidopsis
45	46	52.3	575	2	Q62657	Q62657	rattus norv

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 12, 2005, 10:01:03 ; Search time 118.868 Seconds
                                          (without alignments)
                                          68.328 Million cell updates/sec

Title: US-09-883-839-2-THR42_COPY_35_55
Perfect score: 121
Sequence: 1 SHLDGNLtDPCGPNRTNLGGR 21

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
             1: geneseqp1980s:*
             2: geneseqp1990s:*
             3: geneseqp2000s:*
             4: geneseqp2001s:*
             5: geneseqp2002s:*
             6: geneseqp2003as:*
             7: geneseqp2003bs:*
             8: geneseqp2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     1   117   96.7   392   4   ABB56377   Abb56377 Non-endog
     2   117   96.7   400   2   AAR76780   Aar76780 Human mu
     3   117   96.7   400   3   AAY79946   Aay79946 Human mu
     4   117   96.7   400   3   AAY79949   Aay79949 Human mu
     5   117   96.7   400   3   AAY79945   Aay79945 Human mu
     6   117   96.7   400   3   AAY79947   Aay79947 Human mu
     7   117   96.7   400   4   ABB56376   Abb56376 Non-endog
     8   117   96.7   400   5   AAU76034   Aau76034 Human mu
     9   117   96.7   400   6   ABP81851   Abp81851 Human opi

10	117	96.7	400	8	ADO29588	Ado29588 Human GPC
11·	117	96.7	415	5	ABG33032	Abg33032 Human mu
12	112	92.6	400	2	AAR71966	Aar71966 Human mu
13	112	92.6	400	3	AAY79948	Aay79948 Human mu
14	112	92.6	400	3	AAB07866	Aab07866 A human m
15	112	92.6	400	8	ADH50093	Adh50093 Human mu
16	112	92.6	400	8	ADH50086	Adh50086 Human mu
17	112	92.6	400	8	ADN38673	Adn38673 Wild type
18	112	92.6	400	8	ADR44838	Adr44838 HUMOR mut
19	112	92.6	400	8	ADR44829	Adr44829 Human HUM
20	112	92.6	412	5	ABG32261	Abg32261 Human mu2
21	112	92.6	414	5	ABG32260	Abg32260 Human mu2
22	112	92.6	418	7	ADG42210	Adg42210 Mu-opioid
23	112	92.6	446	7	ADG42209	Adg42209 Mu-opioid
24	112	92.6	462	6	AAE33476	Aae33476 Human REM
25	112	92.6	476	5	ABG32259	Abg32259 Human mu1
26	107	88.4	392	6	AAE33276	Aae33276 Human mod
27	107	88.4	392	6	AAE33275	Aae33275 Human mu
28	107	88.4	399	6	AAE33277	Aae33277 Human mod
29	102	84.3	401	8	ADH50092	Adh50092 Bovine mu
30	102	84.3	401	8	ADR44843	Adr44843 Bovine mu
31	101	83.5	20	6	ABP82456	Abp82456 G protein
32	97	80.2	388	7	ADG42205	Adg42205 Mu-opioid
33	97	80.2	390	3	AAY68885	Aay68885 A murine
34	97	80.2	391	3	AAY68886	Aay68886 A murine
35	97	80.2	392	3	AAY68879	Aay68879 A murine
36	97	80.2	392	7	ADG42206	Adg42206 Mu-opioid
37·	97	80.2	398	2	AAW44937	Aaw44937 Mouse mu
38	97	80.2	398	3	AAY68889	Aay68889 A murine
39	97	80.2	398	8	ADH50091	Adh50091 Mouse mu
40	97	80.2	398	8	ADO29589	Ado29589 Mouse GPC
41	97	80.2	398	8·	ADN38674	Adn38674 Wild type
42	97	80.2	398	8	ADR44831	Adr44831 Mouse HUM
43	97	80.2	398	8	ADR44845	Adr44845 Mouse mu-
44	97	80.2	401	3	AAY68880	Aay68880 A murine
45	97	80.2	409	3	AAY68887	Aay68887 A murine

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:06:54 ; Search time 30.5094 Seconds
                                        (without alignments)
                                        51.382 Million cell updates/sec

Title: US-09-883-839-2-THR42_COPY_35_55
Perfect score: 121
Sequence: 1 SHLDGNLtDPCGPNRTNLGGR 21

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
               1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
               2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
               3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
               4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
               5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB ID   Description
----
     1   117   96.7   392   4 US-09-826-509-547   Sequence 547, App
     2   117   96.7   400   3 US-08-188-275A-2   Sequence 2, Appli
     3   117   96.7   400   3 US-09-351-198-2   Sequence 2, Appli
     4   117   96.7   400   3 US-09-113-426-2   Sequence 2, Appli
     5   117   96.7   400   4 US-09-826-509-545   Sequence 545, App
     6   117   96.7   415   4 US-08-405-271A-20   Sequence 20, Appl
     7   112   92.6   400   3 US-08-889-108-8   Sequence 8, Appli
     8   112   92.6   400   5 PCT-US94-10358-8   Sequence 8, Appli
     9   97   80.2   390   4 US-09-761-962A-25   Sequence 25, Appl
    10   97   80.2   391   4 US-09-761-962A-26   Sequence 26, Appl
    11   97   80.2   392   4 US-09-761-962A-19   Sequence 19, Appl
    12   97   80.2   398   4 US-09-761-962A-29   Sequence 29, Appl
    13   97   80.2   398   4 US-09-214-904-2   Sequence 2, Appli
    14   97   80.2   401   4 US-09-761-962A-20   Sequence 20, Appl
    15   97   80.2   409   4 US-09-761-962A-27   Sequence 27, Appl
    16   97   80.2   438   4 US-09-761-962A-17   Sequence 17, Appl

17	97	80.2	444	4	US-09-761-962A-28	Sequence 28, Appl
18	87	71.9	391	2	US-08-454-549-3	Sequence 3, Appli
19	87	71.9	391	3	US-08-454-552-3	Sequence 3, Appli
20	87	71.9	391	3	US-08-676-351-4	Sequence 4, Appli
21	87	71.9	398	1	US-08-149-093A-5	Sequence 5, Appli
22	87	71.9	398	2	US-08-911-245-5	Sequence 5, Appli
23	87	71.9	398	3	US-09-170-331-5	Sequence 5, Appli
24	87	71.9	398	3	US-08-889-108-2	Sequence 2, Appli
25	87	71.9	398	3	US-08-120-601B-2	Sequence 2, Appli
26	87	71.9	398	3	US-08-188-275A-3	Sequence 3, Appli
27	87	71.9	398	3	US-08-387-707-16	Sequence 16, Appl
28	87	71.9	398	3	US-09-510-473-5	Sequence 5, Appli
29	87	71.9	398	3	US-09-351-198-3	Sequence 3, Appli
30	87	71.9	398	3	US-09-113-426-3	Sequence 3, Appli
31	87	71.9	398	4	US-08-405-271A-16	Sequence 16, Appl
32	87	71.9	398	5	PCT-US94-10358-2	Sequence 2, Appli
33	81	66.9	398	2	US-08-514-451A-8	Sequence 8, Appli
34	81	66.9	398	4	US-09-048-916B-7	Sequence 7, Appli
35	66.5	55.0	19	4	US-09-051-685A-11	Sequence 11, Appl
36	49	40.5	1484	2	US-08-231-193A-56	Sequence 56, Appl
37	49	40.5	1484	2	US-08-486-273A-56	Sequence 56, Appl
38	49	40.5	1484	3	US-08-940-086A-56	Sequence 56, Appl
39	49	40.5	1484	3	US-08-940-035A-56	Sequence 56, Appl
40	49	40.5	1484	3	US-08-935-105A-56	Sequence 56, Appl
41	49	40.5	1484	4	US-09-648-797-56	Sequence 56, Appl
42	49	40.5	1484	4	US-09-386-123-56	Sequence 56, Appl
43	49	40.5	1484	4	US-10-038-937-56	Sequence 56, Appl
44	48	39.7	426	4	US-09-277-196-19	Sequence 19, Appl
45	48	39.7	448	4	US-09-643-597-340	Sequence 340, App

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:09:59 ; Search time 91.5283 Seconds
                                                (without alignments)
                                                76.644 Million cell updates/sec

Title: US-09-883-839-2-THR42_COPY_35_55
Perfect score: 121
Sequence: 1 SHLDGNLtDPCGPNRTNLGGR 21

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
                  1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                  2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                  3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                  4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                  5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                  6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                  7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                  8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                  9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                  10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                  11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                  12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                  13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                  14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                  15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                  16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                  17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                  18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                  19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                  20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB ID   Description
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      1   121 100.0   400 11 US-09-883-839-6   Sequence 6, Appli
      2   117   96.7   392 10 US-09-826-509-547   Sequence 547, App

3	117	96.7	392	17	US-10-925-095-547	Sequence 547, App
4	117	96.7	400	10	US-09-826-509-545	Sequence 545, App
5	117	96.7	400	11	US-09-883-839-2	Sequence 2, Appli
6	117	96.7	400	11	US-09-883-839-4	Sequence 4, Appli
7	117	96.7	400	14	US-10-225-567A-186	Sequence 186, App
8	117	96.7	400	17	US-10-925-095-545	Sequence 545, App
9	117	96.7	401	11	US-09-883-839-10	Sequence 10, Appl
10	117	96.7	415	9	US-09-823-114-20	Sequence 20, Appl
11	117	96.7	415	14	US-10-290-748-20	Sequence 20, Appl
12	112	92.6	400	9	US-09-966-871-78	Sequence 78, Appl
13	112	92.6	400	9	US-09-966-871-85	Sequence 85, Appl
14	112	92.6	400	13	US-10-039-645-78	Sequence 78, Appl
15	112	92.6	400	13	US-10-039-645-85	Sequence 85, Appl
16	112	92.6	400	15	US-10-458-860-78	Sequence 78, Appl
17	112	92.6	400	15	US-10-458-860-85	Sequence 85, Appl
18	112	92.6	400	15	US-10-465-172A-7	Sequence 7, Appli
19	112	92.6	412	14	US-10-080-917-11	Sequence 11, Appl
20	112	92.6	414	14	US-10-080-917-9	Sequence 9, Appli
21	112	92.6	418	14	US-10-185-083-40	Sequence 40, Appl
22	112	92.6	446	14	US-10-185-083-39	Sequence 39, Appl
23	112	92.6	462	17	US-10-477-714-7	Sequence 7, Appli
24	112	92.6	476	14	US-10-080-917-7	Sequence 7, Appli
25	107	88.4	392	10	US-09-935-061-12	Sequence 12, Appl
26	107	88.4	392	10	US-09-935-061-14	Sequence 14, Appl
27	107	88.4	392	16	US-10-692-071-12	Sequence 12, Appl
28	107	88.4	392	16	US-10-692-071-14	Sequence 14, Appl
29	107	88.4	399	10	US-09-935-061-16	Sequence 16, Appl
30	107	88.4	399	16	US-10-692-071-16	Sequence 16, Appl
31	102	84.3	401	15	US-10-458-860-84	Sequence 84, Appl
32	102	84.3	405	9	US-09-966-871-84	Sequence 84, Appl
33	102	84.3	405	13	US-10-039-645-84	Sequence 84, Appl
34	101	83.5	20	14	US-10-225-567A-1129	Sequence 1129, Ap
35	97	80.2	388	14	US-10-185-083-35	Sequence 35, Appl
36	97	80.2	390	9	US-09-761-962-25	Sequence 25, Appl
37	97	80.2	390	14	US-10-283-300-25	Sequence 25, Appl
38	97	80.2	391	9	US-09-761-962-26	Sequence 26, Appl
39	97	80.2	391	14	US-10-283-300-26	Sequence 26, Appl
40	97	80.2	392	9	US-09-761-962-19	Sequence 19, Appl
41	97	80.2	392	14	US-10-185-083-36	Sequence 36, Appl
42	97	80.2	392	14	US-10-283-300-19	Sequence 19, Appl
43	97	80.2	398	9	US-09-214-904-2	Sequence 2, Appli
44	97	80.2	398	9	US-09-761-962-29	Sequence 29, Appl
45	97	80.2	398	9	US-09-966-871-83	Sequence 83, Appl

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:05:49 ; Search time 22.5849 Seconds
                                          (without alignments)
                                          89.465 Million cell updates/sec

Title: US-09-883-839-2-THR42_COPY_35_55
Perfect score: 121
Sequence: 1 SHLDGNLtDPCGPNRTNLGGR 21

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   112   92.6   400   2   I56553   mu opiate receptor
     2   107   88.4   392   2   S65693   opioid receptor mu
     3   97   80.2   398   2   A57510   mu opioid receptor
     4   87   71.9   398   2   I56517   mu opioid receptor
     5   87   71.9   398   2   I56504   mu opioid receptor
     6   53   43.8   2588   2   T14342   NSD1 protein - mou
     7   50   41.3   825   2   S28478   rfbN protein - Vib
     8   50   41.3   825   2   B82347   acyl protein synth
     9   49   40.5   658   2   T08153   cysteine proteinas
    10   48   39.7   334   2   T17213   hypothetical prote
    11   48   39.7   658   2   F71410   hypothetical prote
    12   48   39.7   2055   2   T00093   hypothetical prote
    13   47   38.8   292   2   T00829   wuschel protein -
    14   47   38.8   293   2   D84558   probable homeodoma
    15   47   38.8   569   2   S59398   probable membrane
    16   46   38.0   614   2   A41757   betaine transport
    17   45.5   37.6   837   2   T00355   hypothetical prote
    18   45   37.2   340   2   C95940   probable allantoic

19	45	37.2	755	2	T46411	hypothetical prote
20	45	37.2	886	2	A57172	probable hormone r
21	45	37.2	971	2	H71719	hypothetical prote
22	44	36.4	522	2	T09705	glucose-1-phosphat
23	44	36.4	722	1	VCPVV2	coat protein VP1 -
24	43	35.5	187	2	T10073	amine dehydrogenas
25	43	35.5	299	2	F97544	high-affinity zinc
26	43	35.5	299	2	AG2763	hypothetical prote
27	43	35.5	397	2	JE0082	GPI-linked recepto
28	43	35.5	426	1	T49035	acid phosphatase (
29	43	35.5	534	1	JC1515	calcium-dependent
30	43	35.5	734	2	F88098	protein F18A12.4 [
31	43	35.5	1037	2	D96786	protein F10A5.15 [
32	43	35.5	1441	2	B86807	hypothetical prote
33	43	35.5	1482	2	I49704	glutamate receptor
34	43	35.5	1482	2	B43274	N-methyl-D-asparta
35	43	35.5	1484	2	S52086	N-methyl-D-asparta
36	42.5	35.1	287	2	T05338	hypothetical prote
37	42.5	35.1	2139	2	A35672	crumbs protein - f
38	42	34.7	517	2	S12227	hypothetical prote
39	42	34.7	550	1	A49936	arginine-tRNA liga
40	42	34.7	673	2	S36336	probable transcrip
41	42	34.7	779	2	AE1240	translation initia
42	42	34.7	991	2	T01377	hypothetical prote
43	42	34.7	1338	2	T02206	hypothetical prote
44	42	34.7	1341	2	S50366	probable membrane
45	42	34.7	2505	1	XYRTFA	enoyl-[acyl-carrie

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:04:59 ; Search time 110.151 Seconds
                                          (without alignments)
                                        97.627 Million cell updates/sec

Title: US-09-883-839-2-THR42_COPY_35_55
Perfect score: 121
Sequence: 1 SHLDGNLtDPCGPNRTNLGGR 21

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	92.6	89	2	O43185	O43185 homo sapien
2	112	92.6	400	1	OPRM_HUMAN	P35372 homo sapien
3	112	92.6	400	1	OPRM_MACMU	Q9myw9 macaca mula
4	112	92.6	400	2	Q95M54	Q95m54 macaca fasc
5	112	92.6	402	2	Q6UQ80	Q6uq80 homo sapien
6	112	92.6	418	2	Q8IWW3	Q8iww3 homo sapien
7	112	92.6	446	2	Q8IWW4	Q8iww4 homo sapien
8	112	92.6	454	2	Q9H573	Q9h573 homo sapien
9	102	84.3	401	1	OPRM_BOVIN	P79350 bos taurus
10	98	81.0	400	2	Q8CGM4	Q8cgm4 cavia porce
11	97	80.2	388	2	Q8CH75	Q8ch75 mus musculu
12	97	80.2	390	2	Q8VI71	Q8vi71 mus musculu
13	97	80.2	391	2	Q8VI70	Q8vi70 mus musculu
14	97	80.2	392	2	Q8CH74	Q8ch74 mus musculu
15	97	80.2	393	2	Q9R1M0	Q9r1m0 mus musculu
16	97	80.2	398	1	OPRM_MOUSE	P42866 mus musculu
17	97	80.2	401	2	Q9R1L9	Q9r1l9 mus musculu
18	97	80.2	409	2	Q8VI69	Q8vi69 mus musculu
19	97	80.2	416	2	Q6YC50	Q6yc50 mus musculu
20	97	80.2	425	2	Q8CH73	Q8ch73 mus musculu

21	97	80.2	438	2	Q8CAN5	Q8can5 mus musculu
22	97	80.2	438	2	Q9R0D1	Q9r0d1 mus musculu
23	97	80.2	444	2	Q9JIY1	Q9jiy1 mus musculu
24	97	80.2	456	2	Q8CGW2	Q8cgw2 mus musculu
25	87	71.9	94	2	Q80WZ4	Q80wz4 rattus sp.
26	87	71.9	398	1	OPRM_RAT	P33535 rattus norv
27	83	68.6	401	1	OPRM_PIG	Q95247 sus scrofa
28	53	43.8	699	2	Q9H6H8	Q9h6h8 homo sapien
29	53	43.8	881	2	Q658U6	Q658u6 homo sapien
30	53	43.8	1069	2	Q9H6B5	Q9h6b5 homo sapien
31	53	43.8	2588	2	O88491	O88491 mus musculu
32	53	43.8	2696	1	NSD1_HUMAN	Q96173 homo sapien
33	51	42.1	394	2	Q6PSS8	Q6pss8 uncultured
34	51	42.1	1792	2	O57484	O57484 gallus gall
35	50	41.3	489	2	P72455	P72455 streptomyce
36	50	41.3	586	2	Q6BPI4	Q6bpi4 debaryomyce
37	50	41.3	825	2	Q06961	Q06961 vibrio chol
38	50	41.3	825	2	Q9KV99	Q9kv99 vibrio chol
39	49.5	40.9	369	2	Q6QUF8	Q6quf8 human immun
40	49	40.5	658	2	O65214	O65214 volvox cart
41	48	39.7	241	1	MIA1_SARMU	Q26539 sarcocystis
42	48	39.7	241	1	MIAM_SARMU	Q08668 sarcocystis
43	48	39.7	295	2	Q6RDV5	Q6rdv5 human immun
44	48	39.7	334	2	Q9UFQ8	Q9ufq8 homo sapien
45	48	39.7	338	2	Q7TSS6	Q7tss6 mus musculu

GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein -·protein search, using sw model

Run on: May 12, 2005, 10:01:03 ; Search time 90.566 Seconds
                                        (without alignments)
                                        68.328 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                  %
Result   Query
   No.   Score   Match   Length DB   ID   Description
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     1   80   90.9   392   4   ABB56377   Abb56377 Non-endog
     2   80   90.9   392   6   AAE33276   Aae33276 Human mod
     3   80   90.9   392   6   AAE33275   Aae33275 Human mu
     4   80   90.9   399. 6   AAE33277   Aae33277 Human mod
     5   80   90.9   400   2   AAR71966   Aar71966 Human mu
     6   80   90.9   400   2   AAR76780   Aar76780 Human mu
     7   80   90.9   400   3   AAY79946   Aay79946 Human mu
     8   80   90.9   400   3   AAY79949   Aay79949 Human mu
     9   80   90.9   400   3   AAY79945   Aay79945 Human mu
    10   80   90.9   400   3   AAY79948   Aay79948 Human mu

11	80	90.9	400	3	AAY79947	Aay79947	Human mu
12	80	90.9	400	3	AAB07866	Aab07866	A human m
13	80	90.9	400	4	ABB56376	Abb56376	Non-endog
14	80	90.9	400	5	AAU76034	Aau76034	Human mu
15	80	90.9	400	6	ABP81851	Abp81851	Human opi
16	80	90.9	400	8	ADH50093	Adh50093	Human mu
17	80	90.9	400	8	ADH50086	Adh50086	Human mu
18	80	90.9	400	8	ADO29588	Ado29588	Human GPC
19	80	90.9	400	8	ADN38673	Adn38673	Wild type
20	80	90.9	400	8	ADR44838	Adr44838	HUMOR mut
21	80	90.9	400	8	ADR44829	Adr44829	Human HUM
22	80	90.9	414	5	ABG32260	Abg32260	Human mu2
23	80	90.9	415	5	ABG33032	Abg33032	Human mu
24	80	90.9	418	7	ADG42210	Adg42210	Mu-opioid
25	80	90.9	446	7	ADG42209	Adg42209	Mu-opioid
26	80	90.9	462	6	AAE33476	Aae33476	Human REM
27	80	90.9	476	5	ABG32259	Abg32259	Human mu1
28	52	59.1	45	4	AAG77039	Aag77039	Human col
29	52	59.1	136	8	ADG22372	Adg22372	Cyanophag
30	52	59.1	808	8	ADO63031	Ado63031	Transcrip
31	51	58.0	62	3	AAY95586	Aay95586	Prostate
32	51	58.0	423	4	ABG16849	Abg16849	Novel hum
33	51	58.0	1085	4	ABG08327	Abg08327	Novel hum
34	50	56.8	182	4	AAU29831	Aau29831	Novel hum
35	50	56.8	398	4	ABB70325	Abb70325	Drosophil
36	50	56.8	426	4	ABB67253	Abb67253	Drosophil
37	50	56.8	1682	8	ADR14131	Adr14131	Human NF-
38	49.5	56.2	697	8	ADQ65928	Adq65928	Novel hum
39	49.5	56.2	938	6	ABP98888	Abp98888	Human mol
40	49.5	56.2	1047	5	ABG31634	Abg31634	Human PHP
41	49.5	56.2	1047	8	ADQ65756	Adq65756	Novel hum
42	49.5	56.2	1047	8	ADQ66302	Adq66302	Novel hum
43	49.5	56.2	1047	8	ADR09925	Adr09925	Human pro
44	49	55.7	401	8	ADH50092	Adh50092	Bovine mu
45	49	55.7	401	8	ADR44843	Adr44843	Bovine mu

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:06:54 ; Search time 23.2453 Seconds
                                        (without alignments)
                                        51.382 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
      1   80   90.9   392   4   US-09-826-509-547   Sequence 547, App
      2   80   90.9   400   3   US-08-889-108-8   Sequence 8, Appli
      3   80   90.9   400   3   US-08-188-275A-2   Sequence 2, Appli
      4   80   90.9   400   3   US-09-351-198-2   Sequence 2, Appli
      5   80   90.9   400   3   US-09-113-426-2   Sequence 2, Appli
      6   80   90.9   400   4   US-09-826-509-545   Sequence 545, App
      7   80   90.9   400   5   PCT-US94-10358-8   Sequence 8, Appli
      8   80   90.9   415   4   US-08-405-271A-20   Sequence 20, Appl
      9   48   54.5   404   2   US-08-282-197C-62   Sequence 62, Appl
     10   48   54.5   405   4   US-09-252-991A-30240   Sequence 30240, A
     11   47   53.4   411   2· US-08-440-845D-3   Sequence 3, Appli
     12   47   53.4   411   3   US-08-868-458-3   Sequence 3, Appli
     13   46   52.3   83   4   US-09-270-767-35053   Sequence 35053, A
     14   46   52.3   83   4   US-09-270-767-50270   Sequence 50270, A
     15   46   52.3   89   4   US-09-489-039A-9922   Sequence 9922, Ap
     16   46   52.3   134   4   US-09-252-991A-26710   Sequence 26710, A

17	46	52.3	155	4	US-09-489-039A-9198	Sequence 9198, Ap
18	46	52.3	408	4	US-09-252-991A-24424	Sequence 24424, A
19	46	52.3	591	4	US-09-252-991A-24904	Sequence 24904, A
20	46	52.3	989	2	US-08-070-301-14	Sequence 14, Appl
21	45	51.1	102	4	US-09-513-999C-7547	Sequence 7547, Ap
22	45	51.1	136	4	US-09-252-991A-29563	Sequence 29563, A
23	45	51.1	538	4	US-09-252-991A-22200	Sequence 22200, A
24	44.5	50.6	169	1	US-08-310-416A-18	Sequence 18, Appl
25	44.5	50.6	169	2	US-08-888-171-18	Sequence 18, Appl
26	44.5	50.6	254	1	US-08-310-416A-13	Sequence 13, Appl
27	44.5	50.6	254	2	US-08-888-171-13	Sequence 13, Appl
28	44.5	50.6	254	2	US-08-435-149-1	Sequence 1, Appli
29	44.5	50.6	279	4	US-09-331-793-25	Sequence 25, Appl
30	44.5	50.6	293	1	US-08-310-416A-16	Sequence 16, Appl
31	44.5	50.6	293	2	US-08-888-171-16	Sequence 16, Appl
32	44.5	50.6	324	2	US-08-528-057-46	Sequence 46, Appl
33	44.5	50.6	369	4	US-09-949-016-6217	Sequence 6217, Ap
34	44.5	50.6	370	2	US-08-528-057-42	Sequence 42, Appl
35	44.5	50.6	373	2	US-08-528-057-44	Sequence 44, Appl
36	44.5	50.6	377	2	US-08-528-057-2	Sequence 2, Appli
37	44.5	50.6	384	3	US-08-139-195-2	Sequence 2, Appli
38	44.5	50.6	384	6	5514787-2	Patent No. 5514787
39	44.5	50.6	384	6	5514787-2	Patent No. 5514787
40	44.5	50.6	577	2	US-08-435-149-3	Sequence 3, Appli
41	44.5	50.6	611	3	US-09-475-460A-32	Sequence 32, Appl
42	44.5	50.6	611	4	US-09-748-061A-32	Sequence 32, Appl
43	44	50.0	503	4	US-09-599-287A-2	Sequence 2, Appli
44	44	50.0	506	4	US-09-949-016-11282	Sequence 11282, A
45	44	50.0	507	4	US-09-599-287A-24	Sequence 24, Appl

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:06:54 ; Search time 23.2453 Seconds
                                        (without alignments)
                                        51.382 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                   SUMMARIES
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Result   Query
  No.   Score   Match Length DB ID   Description
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      4   80   90.9   400 3 US-09-351-198-2   Sequence 2, Appli
      5   80   90.9   400 3 US-09-113-426-2   Sequence 2, Appli
      6   80   90.9   400 4 US-09-826-509-545   Sequence 545, App
      7   80   90.9   400 5 PCT-US94-10358-8   Sequence 8, Appli
      8   80   90.9   415 4 US-08-405-271A-20   Sequence 20, Appl
      9   48   54.5   404 2 US-08-282-197C-62   Sequence 62, Appl
     10   48   54.5   405 4 US-09-252-991A-30240   Sequence 30240, A
     11   47   53.4   411 2 US-08-440-845D-3   Sequence 3, Appli
     12   47   53.4   411 3 US-08-868-458-3   Sequence 3, Appli
     13   46   52.3   83 4 US-09-270-767-35053   Sequence 35053, A
     14   46   52.3   83 4 US-09-270-767-50270   Sequence 50270, A
     15   46   52.3   89 4 US-09-489-039A-9922   Sequence 9922, Ap
     16   46   52.3   134 4 US-09-252-991A-26710   Sequence 26710, A

17	46	52.3	155	4	US-09-489-039A-9198	Sequence 9198, Ap
18	46	52.3	408	4	US-09-252-991A-24424	Sequence 24424, A
19	46	52.3	591	4	US-09-252-991A-24904	Sequence 24904, A
20	46	52.3	989	2	US-08-070-301-14	Sequence 14, Appl
21	45	51.1	102	4	US-09-513-999C-7547	Sequence 7547, Ap
22	45	51.1	136	4	US-09-252-991A-29563	Sequence 29563, A
23	45	51.1	538	4	US-09-252-991A-22200	Sequence 22200, A
24	44.5	50.6	169	1	US-08-310-416A-18	Sequence 18, Appl
25	44.5	50.6	169	2	US-08-888-171-18	Sequence 18, Appl
26	44.5	50.6	254	1	US-08-310-416A-13	Sequence 13, Appl
27	44.5	50.6	254	2	US-08-888-171-13	Sequence 13, Appl
28	44.5	50.6	254	2	US-08-435-149-1	Sequence 1, Appli
29	44.5	50.6	279	4	US-09-331-793-25	Sequence 25, Appl
30	44.5	50.6	293	1	US-08-310-416A-16	Sequence 16, Appl
31	44.5	50.6	293	2	US-08-888-171-16	Sequence 16, Appl
32	44.5	50.6	324	2	US-08-528-057-46	Sequence 46, Appl
33	44.5	50.6	369	4	US-09-949-016-6217	Sequence 6217, Ap
34	44.5	50.6	370	2	US-08-528-057-42	Sequence 42, Appl
35	44.5	50.6	373	2	US-08-528-057-44	Sequence 44, Appl
36	44.5	50.6	377	2	US-08-528-057-2	Sequence 2, Appli
37	44.5	50.6	384	3	US-08-139-195-2	Sequence 2, Appli
38	44.5	50.6	384	6	5514787-2	Patent No. 5514787
39	44.5	50.6	384	6	5514787-2	Patent No. 5514787
40	44.5	50.6	577	2	US-08-435-149-3	Sequence 3, Appli
41	44.5	50.6	611	3	US-09-475-460A-32	Sequence 32, Appl
42	44.5	50.6	611	4	US-09-748-061A-32	Sequence 32, Appl
43	44	50.0	503	4	US-09-599-287A-2	Sequence 2, Appli
44	44	50.0	506	4	US-09-949-016-11282	Sequence 11282, A
45	44	50.0	507	4	US-09-599-287A-24	Sequence 24, Appl

Run on: May 12, 2005, 10:09:59 ; Search time 69.7358 Seconds
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                                          76.644 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
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                 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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                 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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                 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
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     2   80   90.9   392 10 US-09-935-061-12   Sequence 12, Appl
     3   80   90.9   392 10 US-09-935-061-14   Sequence 14, Appl

4	80	90.9	392	10	US-09-826-509-547	Sequence 547, App
5	80	90.9	392	16	US-10-692-071-12	Sequence 12, Appl
6	80	90.9	392	16	US-10-692-071-14	Sequence 14, Appl
7	80	90.9	392	17	US-10-925-095-547	Sequence 547, App
8	80	90.9	399	10	US-09-935-061-16	Sequence 16, Appl
9	80	90.9	399	16	US-10-692-071-16	Sequence 16, Appl
10	80	90.9	400	9	US-09-966-871-78	Sequence 78, Appl
11	80	90.9	400	9	US-09-966-871-85	Sequence 85, Appl
12	80	90.9	400	10	US-09-826-509-545	Sequence 545, App
13	80	90.9	400	11	US-09-883-839-2	Sequence 2, Appli
14	80	90.9	400	11	US-09-883-839-6	Sequence 6, Appli
15	80	90.9	400	13	US-10-039-645-78	Sequence 78, Appl
16	80	90.9	400	13	US-10-039-645-85	Sequence 85, Appl
17	80	90.9	400	14	US-10-225-567A-186	Sequence 186, App
18	80	90.9	400	15	US-10-458-860-78	Sequence 78, Appl
19	80	90.9	400	15	US-10-458-860-85	Sequence 85, Appl
20	80	90.9	400	15	US-10-465-172A-7	Sequence 7, Appli
21	80	90.9	400	17	US-10-925-095-545	Sequence 545, App
22	80	90.9	401	11	US-09-883-839-10	Sequence 10, Appl
23	80	90.9	414	14	US-10-080-917-9	Sequence 9, Appli
24	80	90.9	415	9	US-09-823-114-20	Sequence 20, Appl
25	80	90.9	415	14	US-10-290-748-20	Sequence 20, Appl
26	80	90.9	418	14	US-10-185-083-40	Sequence 40, Appl
27	80	90.9	446	14	US-10-185-083-39	Sequence 39, Appl
28	80	90.9	462	17	US-10-477-714-7	Sequence 7, Appli
29	80	90.9	476	14	US-10-080-917-7	Sequence 7, Appli
30	52	59.1	45	14	US-10-106-698-7813	Sequence 7813, Ap
31	50	56.8	140	16	US-10-437-963-163725	Sequence 163725,
32	50	56.8	168	15	US-10-424-599-241575	Sequence 241575,
33	50	56.8	402	16	US-10-437-963-150861	Sequence 150861,
34	50	56.8	1682	16	US-10-755-889-132	Sequence 132, App
35	49.5	56.2	1047	17	US-10-468-026-2	Sequence 2, Appli
36	49	55.7	125	16	US-10-437-963-104313	Sequence 104313,
37	49	55.7	154	16	US-10-437-963-177487	Sequence 177487,
38	49	55.7	219	16	US-10-437-963-201051	Sequence 201051,
39	49	55.7	401	15	US-10-458-860-84	Sequence 84, Appl
40	49	55.7	405	9	US-09-966-871-84	Sequence 84, Appl
41	49	55.7	405	13	US-10-039-645-84	Sequence 84, Appl
42	49	55.7	476	15	US-10-282-122A-67940	Sequence 67940, A
43	48	54.5	252	14	US-10-029-386-34071	Sequence 34071, A
44	47	53.4	120	9	US-09-854-286-4	Sequence 4, Appli
45	47	53.4	122	9	US-09-764-877-1299	Sequence 1299, Ap

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:05:49 ; Search time 17.2075 Seconds
                                      (without alignments)
                                      89.465 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
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               3: pir3:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
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   No.   Score   Match Length DB   ID   Description
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     2   80   90.9   400   2   I56553   mu opiate receptor
     3   52   59.1   808   2   A96791   hypothetical prote
     4   50   56.8   183   2   T49855   hypothetical prote
     5   48   54.5   744   2   E86255   hypothetical prote
     6   47   53.4   240   2   E72629   hypothetical prote
     7   47   53.4   1185   2   T46428   hypothetical prote
     8   46   52.3   553   2   G83385   hypothetical prote
     9   46   52.3   592   2   T03682   catechol oxidase (
    10   46   52.3   972   1   URBOAP   peptidylglycine mo
    11   45.5   51.7   262   2   F84505   probable bZIP tran
    12   45.5   51.7   294   2   G84504   probable VSF-1-lik
    13   45   51.1   388   2   S25298   extensin (clone To
    14   45   51.1   403   2   G96548   hypothetical prote
    15   45   51.1   487   2   T49424   hypothetical prote
    16   44.5   50.6   349   2   G02913   sperm CD46 - human
    17   44.5   50.6   362   2   JC5194   membrane cofactor
    18   44.5   50.6   369   2   I57998   membrane cofactor

19	44.5	50.6	369	2	JC5138	membrane cofactor
20	44.5	50.6	377	2	I54479	membrane cofactor
21	44.5	50.6	384	2	S01896	membrane cofactor
22	44	50.0	403	2	S52796	prpL2 protein - hu
23	44	50.0	403	2	T51828	probable photosyst
24	44	50.0	647	2	T43952	hypothetical prote
25	44	50.0	759	2	T44142	DR1 protein [impor
26	44	50.0	775	2	I49759	hepatocyte growth
27	44	50.0	1459	2	T30196	kinesin motor prot
28	43	48.9	182	2	B35650	hypothetical 20K p
29	43	48.9	223	2	AD2793	conserved hypothet
30	43	48.9	261	2	B97572	hypothetical prote
31	43	48.9	261	2	JQ0319	hypothetical 27K p
32	43	48.9	322	1	HLHUR2	T-cell surface gly
33	43	48.9	335	2	T20465	hypothetical prote
34	43	48.9	398	2	I56517	mu opioid receptor
35	43	48.9	398	2	I56504	mu opioid receptor
36	43	48.9	408	2	T43240	CBS-domain protein
37	43	48.9	595	1	TVCHRL	transforming prote
38	43	48.9	598	2	S10893	transforming prote
39	43	48.9	760	2	T06291	extensin homolog T
40	43	48.9	810	1	A33380	interleukin-4 rece
41	42	47.7	118	2	C72490	hypothetical prote
42	42	47.7	137	2	T22308	hypothetical prote
43	42	47.7	182	2	T02170	hypothetical prote
44	42	47.7	200	2	S35292	hypothetical prote
45	42	47.7	212	2	AD2695	conserved hypothet

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:04:59 ; Search time 83.9245 Seconds
                                          (without alignments)
                                          97.627 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
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Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
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                              SUMMARIES
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     4   80   90.9   418 2   Q8IWW3   Q8iww3 homo sapien
     5   80   90.9   446 2   Q8IWW4   Q8iww4 homo sapien
     6   80   90.9   454 2   Q9H573   Q9h573 homo sapien
     7   75   85.2   400 2   Q95M54   Q95m54 macaca fasc
     8   66   75.0   400 1   OPRM_MACMU   Q9myw9 macaca mula
     9   60   68.2   400 2   Q8CGM4   Q8cgm4 cavia porce
    10   53.5   60.8   677 2   Q8BNT0   Q8bnt0 mus musculu
    11   52   59.1   808 2   Q9SFW8   Q9sfw8 arabidopsis
    12   50   56.8   183 2   Q7RU29   Q7ru29 neurospora
    13   50   56.8   398 2   Q9W4Q1   Q9w4q1 drosophila
    14   50   56.8   1682 2   O15054   O15054 homo sapien
    15   49.5   56.2   892 2   Q71JB1   Q71jb1 homo sapien
    16   49.5   56.2   1047 2   Q96FB6   Q96fb6 homo sapien
    17   49.5   56.2   1047 2   Q6ZRI6   Q6zri6 homo sapien
    18   49   55.7   182 2   Q6XQ03   Q6xq03 simian t-ly
    19   49   55.7   345 2   Q6RUK7   Q6ruk7 triticum mo
    20   49   55.7   401 1   OPRM_BOVIN   P79350 bos taurus

21	49	55.7	438	2	Q9Y2B5		Q9y2b5 homo sapien
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23	49	55.7	791	2	Q712J1		Q712j1 rattus norv
24	49	55.7	792	1	KFC2_MOUSE		O08672 mus musculu
25	48	54.5	321	2	Q9GRJ9		Q9grj9 leishmania
26	48	54.5	385	2	Q72H19		Q72h19 thermus the
27	48	54.5	409	2	Q6ZTV6		Q6ztv6 homo sapien
28	48	54.5	504	2	Q751U0		Q751u0 ashbya goss
29	48	54.5	652	2	O54859		O54859 rattus norv
30	48	54.5	744	2	O65375		O65375 arabidopsis
31	48	54.5	822	2	Q84LM0		Q84lm0 cucurbita m
32	47	53.4	235	2	Q8SV14		Q8sv14 encephalito
33	47	53.4	240	2	Q9YBV7		Q9ybv7 aeropyrum p
34	47	53.4	411	2	Q39554		Q39554 cuphea palu
35	47	53.4	574	2	Q9NVB3		Q9nvb3 homo sapien
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37	47	53.4	939	2	Q7SD71		Q7sd71 neurospora
38	47	53.4	1068	1	DAM2_MOUSE		Q80u19 mus musculu
39	47	53.4	1115	2	Q6TAB7		Q6tab7 mus musculu
40	47	53.4	1185	2	Q9NTD2		Q9ntd2 homo sapien
41	47	53.4	1329	2	Q86VY3		Q86vy3 homo sapien
42	47	53.4	1579	2	Q7QIP2		Q7qip2 anopheles g
43	47	53.4	1994	2	Q6ZPP2		Q6zpp2 mus musculu
44	47	53.4	2176	2	Q6V4S5		Q6v4s5 mus musculu
45	47	53.4	2217	2	Q8AV57		Q8av57 gallus gall

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:01:03 ; Search time 90.566 Seconds
                                         (without alignments)
                                         68.328 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	90.9	392	4	ABB56377	Abb56377 Non-endog
2	80	90.9	392	6	AAE33276	Aae33276 Human mod
3	80	90.9	392	6	AAE33275	Aae33275 Human mu
4	80	90.9	399	6	AAE33277	Aae33277 Human mod
5	80	90.9	400	2	AAR71966	Aar71966 Human mu
6	80	90.9	400	2	AAR76780	Aar76780 Human mu
7	80	90.9	400	3	AAY79946	Aay79946 Human mu
8	80	90.9	400	3	AAY79949	Aay79949 Human mu
9	80	90.9	400	3	AAY79945	Aay79945 Human mu
10	80	90.9	400	3	AAY79948	Aay79948 Human mu
11	80	90.9	400	3	AAY79947	Aay79947 Human mu
12	80	90.9	400	3	AAB07866	Aab07866 A human m
13	80	90.9	400	4	ABB56376	Abb56376 Non-endog
14	80	90.9	400	5	AAU76034	Aau76034 Human mu

15	80	90.9	400	6	ABP81851	Abp81851 Human opi
16	80	90.9	400	8	ADH50093	Adh50093 Human mu
17	80	90.9	400	8	ADH50086	Adh50086 Human mu
18	80	90.9	400	8	ADO29588	Ado29588 Human GPC
19	80	90.9	400	8	ADN38673	Adn38673 Wild type
20	80	90.9	400	8	ADR44838	Adr44838 HUMOR mut
21	80	90.9	400	8	ADR44829	Adr44829 Human HUM
22	80	90.9	414	5	ABG32260	Abg32260 Human mu2
23	80	90.9	415	5	ABG33032	Abg33032 Human mu
24	80	90.9	418	7	ADG42210	Adg42210 Mu-opioid
25	80	90.9	446	7	ADG42209	Adg42209 Mu-opioid
26	80	90.9	462	6	AAE33476	Aae33476 Human REM
27	80	90.9	476	5	ABG32259	Abg32259 Human mu1
28	52	59.1	45	4	AAG77039	Aag77039 Human col
29	52	59.1	136	8	ADG22372	Adg22372 Cyanophag
30	52	59.1	808	8	ADO63031	Ado63031 Transcrip
31	51	58.0	62	3	AAY95586	Aay95586 Prostate
32	51	58.0	423	4	ABG16849	Abg16849 Novel hum
33	51	58.0	1085	4	ABG08327	Abg08327 Novel hum
34	50	56.8	182	4	AAU29831	Aau29831 Novel hum
35	50	56.8	398	4	ABB70325	Abb70325 Drosophil
36	50	56.8	426	4	ABB67253	Abb67253 Drosophil
37	50	56.8	1682	8	ADR14131	Adr14131 Human NF-
38	49.5	56.2	697	8	ADQ65928	Adq65928 Novel hum
39	49.5	56.2	938	6	ABP98888	Abp98888 Human mol
40	49.5	56.2	1047	5	ABG31634	Abg31634 Human PHP
41	49.5	56.2	1047	8	ADQ65756	Adq65756 Novel hum
42	49.5	56.2	1047	8	ADQ66302	Adq66302 Novel hum
43	49.5	56.2	1047	8	ADR09925	Adr09925 Human pro
44	49	55.7	401	8	ADH50092	Adh50092 Bovine mu
45	49	55.7	401	8	ADR44843	Adr44843 Bovine mu

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:06:54 ; Search time 23.2453 Seconds
                                        (without alignments)
                                        51.382 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

		%				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	80	90.9	392	4	US-09-826-509-547	Sequence 547, App
2	80	90.9	400	3	US-08-889-108-8	Sequence 8, Appli
3	80	90.9	400	3	US-08-188-275A-2	Sequence 2, Appli
4	80	90.9	400	3	US-09-351-198-2	Sequence 2, Appli
5	80	90.9	400	3	US-09-113-426-2	Sequence 2, Appli
6	80	90.9	400	4	US-09-826-509-545	Sequence 545, App
7	80	90.9	400	5	PCT-US94-10358-8	Sequence 8, Appli
8	80	90.9	415	4	US-08-405-271A-20	Sequence 20, Appl
9	48	54.5	404	2	US-08-282-197C-62	Sequence 62, Appl
10	48	54.5	405	4	US-09-252-991A-30240	Sequence 30240, A
11	47	53.4	411	2	US-08-440-845D-3	Sequence 3, Appli
12	47	53.4	411	3	US-08-868-458-3	Sequence 3, Appli
13	46	52.3	83	4	US-09-270-767-35053	Sequence 35053, A
14	46	52.3	83	4	US-09-270-767-50270	Sequence 50270, A
15	46	52.3	89	4	US-09-489-039A-9922	Sequence 9922, Ap
16	46	52.3	134	4	US-09-252-991A-26710	Sequence 26710, A

17	46	52.3	155	4	US-09-489-039A-9198	Sequence 9198, Ap
18	46	52.3	408	4	US-09-252-991A-24424	Sequence 24424, A
19	46	52.3	591	4	US-09-252-991A-24904	Sequence 24904, A
20	46	52.3	989	2	US-08-070-301-14	Sequence 14, Appl
21	45	51.1	102	4	US-09-513-999C-7547	Sequence 7547, Ap
22	45	51.1	136	4	US-09-252-991A-29563	Sequence 29563, A
23	45	51.1	538	4	US-09-252-991A-22200	Sequence 22200, A
24	44.5	50.6	169	1	US-08-310-416A-18	Sequence 18, Appl
25	44.5	50.6	169	2	US-08-888-171-18	Sequence 18, Appl
26	44.5	50.6	254	1	US-08-310-416A-13	Sequence 13, Appl
27	44.5	50.6	254	2	US-08-888-171-13	Sequence 13, Appl
28	44.5	50.6	254	2	US-08-435-149-1	Sequence 1, Appli
29	44.5	50.6	279	4	US-09-331-793-25	Sequence 25, Appl
30	44.5	50.6	293	1	US-08-310-416A-16	Sequence 16, Appl
31	44.5	50.6	293	2	US-08-888-171-16	Sequence 16, Appl
32	44.5	50.6	324	2	US-08-528-057-46	Sequence 46, Appl
33	44.5	50.6	369	4	US-09-949-016-6217	Sequence 6217, Ap
34	44.5	50.6	370	2	US-08-528-057-42	Sequence 42, Appl
35	44.5	50.6	373	2	US-08-528-057-44	Sequence 44, Appl
36	44.5	50.6	377	2	US-08-528-057-2	Sequence 2, Appli
37	44.5	50.6	384	3	US-08-139-195-2	Sequence 2, Appli
38	44.5	50.6	384	6	5514787-2	Patent No. 5514787
39	44.5	50.6	384	6	5514787-2	Patent No. 5514787
40	44.5	50.6	577	2	US-08-435-149-3	Sequence 3, Appli
41	44.5	50.6	611	3	US-09-475-460A-32	Sequence 32, Appl
42	44.5	50.6	611	4	US-09-748-061A-32	Sequence 32, Appl
43	44	50.0	503	4	US-09-599-287A-2	Sequence 2, Appli
44	44	50.0	506	4	US-09-949-016-11282	Sequence 11282, A
45	44	50.0	507	4	US-09-599-287A-24	Sequence 24, Appl

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:09:59 ; Search time 69.7358 Seconds
                                        (without alignments)
                                        76.644 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
        1:   /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
        2:   /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
        3:   /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
        4:   /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
        5:   /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
        6:   /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
        7:   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
        8:   /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
        9:   /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
        10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
        11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
        12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
        13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
        14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
        15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
        16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
        17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
        18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
        19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
        20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                  %
Result   Query
   No.   Score Match Length DB   ID   Description
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     1   88   100.0   400   11   US-09-883-839-4   Sequence 4, Appli
     2   80   90.9   392   10   US-09-935-061-12   Sequence 12, Appl

3	80	90.9	392	10	US-09-935-061-14	Sequence 14, Appl
4	80	90.9	392	10	US-09-826-509-547	Sequence 547, App
5	80	90.9	392	16	US-10-692-071-12	Sequence 12, Appl
6	80	90.9	392	16	US-10-692-071-14	Sequence 14, Appl
7	80	90.9	392	17	US-10-925-095-547	Sequence 547, App
8	80	90.9	399	10	US-09-935-061-16	Sequence 16, Appl
9	80	90.9	399	16	US-10-692-071-16	Sequence 16, Appl
10	80	90.9	400	9	US-09-966-871-78	Sequence 78, Appl
11	80	90.9	400	9	US-09-966-871-85	Sequence 85, Appl
12	80	90.9	400	10	US-09-826-509-545	Sequence 545, App
13	80	90.9	400	11	US-09-883-839-2	Sequence 2, Appli
14	80	90.9	400	11	US-09-883-839-6	Sequence 6, Appli
15	80	90.9	400	13	US-10-039-645-78	Sequence 78, Appl
16	80	90.9	400	13	US-10-039-645-85	Sequence 85, Appl
17	80	90.9	400	14	US-10-225-567A-186	Sequence 186, App
18	80	90.9	400	15	US-10-458-860-78	Sequence 78, Appl
19	80	90.9	400	15	US-10-458-860-85	Sequence 85, Appl
20	80	90.9	400	15	US-10-465-172A-7	Sequence 7, Appli
21	80	90.9	400	17	US-10-925-095-545	Sequence 545, App
22	80	90.9	401	11	US-09-883-839-10	Sequence 10, Appl
23	80	90.9	414	14	US-10-080-917-9	Sequence 9, Appli
24	80	90.9	415	9	US-09-823-114-20	Sequence 20, Appl
25	80	90.9	415	14	US-10-290-748-20	Sequence 20, Appl
26	80	90.9	418	14	US-10-185-083-40	Sequence 40, Appl
27	80	90.9	446	14	US-10-185-083-39	Sequence 39, Appl
28	80	90.9	462	17	US-10-477-714-7	Sequence 7., Appli
29	80	90.9	476	14	US-10-080-917-7	Sequence 7, Appli
30	52	59.1	45	14	US-10-106-698-7813	Sequence 7813, Ap
31	50	56.8	140	16	US-10-437-963-163725	Sequence 163725,
32	50	56.8	168	15	US-10-424-599-241575	Sequence 241575,
33	50	56.8	402	16	US-10-437-963-150861	Sequence 150861,
34	50	56.8	1682	16	US-10-755-889-132	Sequence 132, App
35	49.5	56.2	1047	17	US-10-468-026-2	Sequence 2, Appli
36	49	55.7	125	16	US-10-437-963-104313	Sequence 104313,
37	49	55.7	154	16	US-10-437-963-177487	Sequence 177487,
38	49	55.7	219	16	US-10-437-963-201051	Sequence 201051,
39	49	55.7	401	.15	US-10-458-860-84	Sequence 84, Appl
40	49	55.7	405	9	US-09-966-871-84	Sequence 84, Appl
41	49	55.7	405	13	US-10-039-645-84	Sequence 84, Appl
42	49	55.7	476	15	US-10-282-122A-67940	Sequence 67940, A
43	48	54.5	252	.14	US-10-029-386-34071	Sequence 34071, A
44	47	53.4	120	9	US-09-854-286-4	Sequence 4, Appli
45	47	53.4	122	9	US-09-764-877-1299	Sequence 1299, Ap

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:05:49 ; Search time 17.2075 Seconds
                                          (without alignments)
                                          89.465 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
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     1   80   90.9   392 2   S65693   opioid receptor mu
     2   80   90.9   400 2   I56553   mu opiate receptor
     3   52   59.1   808 2   A96791   hypothetical prote
     4   50   56.8   183 2   T49855   hypothetical prote
     5   48   54.5   744 2   E86255   hypothetical prote
     6   47   53.4   240 2   E72629   hypothetical prote
     7   47   53.4   1185 2   T46428   hypothetical prote
     8   46   52.3   553 2   G83385   hypothetical prote
     9   46   52.3   592 2   T03682   catechol oxidase (
    10   46   52.3   972 1   URBOAP   peptidylglycine mo
    11   45.5   51.7   262 2   F84505   probable bZIP tran
    12   45.5   51.7   294 2   G84504   probable VSF-1-lik
    13   45   51.1   388 2   S25298   extensin (clone To
    14   45   51.1   403 2   G96548   hypothetical prote
    15   45   51.1   487 2   T49424   hypothetical prote
    16   44.5   50.6   349 2   G02913   sperm CD46 - human
    17   44.5   50.6   362 2   JC5194   membrane cofactor
    18   44.5   50.6   369 2   I57998   membrane cofactor

19	44.5	50.6	369	2	JC5138	membrane cofactor
20	44.5	50.6	377	2	I54479	membrane cofactor
21	44.5	50.6	384	2	S01896	membrane cofactor
22	44	50.0	403	2	S52796	prpL2 protein - hu
23	44	50.0	403	2	T51828	probable photosyst
24	44	50.0	647	2	T43952	hypothetical prote
25	44	50.0	759	2	T44142	DR1 protein [impor
26	44	50.0	775	2	I49759	hepatocyte growth
27	44	50.0	1459	2	T30196	kinesin motor prot
28	43	48.9	182	2	B35650	hypothetical 20K p
29	43	48.9	223	2	AD2793	conserved hypothet
30	43	48.9	261	2	B97572	hypothetical prote
31	43	48.9	261	2	JQ0319	hypothetical 27K p
32	43	48.9	322	1	HLHUR2	T-cell surface gly
33	43	48.9	335	2	T20465	hypothetical prote
34	43	48.9	398	2	I56517	mu opioid receptor
35	43	48.9	398	2	I56504	mu opioid receptor
36	43	48.9	408	2	T43240	CBS-domain protein
37	43	48.9	595	1	TVCHRL	transforming prote
38	43	48.9	598	2	S10893	transforming prote
39	43	48.9	760	2	T06291	extensin homolog T
40	43	48.9	810	1	A33380	interleukin-4 rece
41	42	47.7	118	2	C72490	hypothetical prote
42	42	47.7	137	2	T22308	hypothetical prote
43	42	47.7	182	2	T02170	hypothetical prote
44	42	47.7	200	2	S35292	hypothetical prote
45	42	47.7	212	2	AD2695	conserved hypothet

OM protein - protein search, using sw model

Run on: May 12, 2005, 10:04:59 ; Search time 83.9245 Seconds
                                          (without alignments)
                                          97.627 Million cell updates/sec

Title: US-09-883-839-2-PRO23_COPY_15_30
Perfect score: 88
Sequence: 1 DALAYSSCpPAPSPGS 16

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB   ID   Description
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     1   80   90.9   89 2   O43185   O43185 homo sapien
     2   80   90.9   400 1   OPRM_HUMAN   P35372 homo sapien
     3   80   90.9   402 2   Q6UQ80   Q6uq80 homo sapien
     4   80   90.9   418 2   Q8IWW3   Q8iww3 homo sapien
     5   80   90.9   446 2   Q8IWW4   Q8iww4 homo sapien
     6   80   90.9   454 2   Q9H573   Q9h573 homo sapien
     7   75   85.2   400 2   Q95M54   Q95m54 macaca fasc
     8   66   75.0   400 1   OPRM_MACMU   Q9myw9 macaca mula
     9   60   68.2   400 2   Q8CGM4   Q8cgm4 cavia porce
    10   53.5   60.8   677 2   Q8BNT0   Q8bnt0 mus musculu
    11   52   59.1   808 2   Q9SFW8   Q9sfw8 arabidopsis
    12   50   56.8   183 2   Q7RU29   Q7ru29 neurospora
    13   50   56.8   398 2   Q9W4Q1   Q9w4q1 drosophila
    14   50   56.8   1682 2   O15054   O15054 homo sapien
    15   49.5   56.2   892 2   Q71JB1   Q71jb1 homo sapien
    16   49.5   56.2   1047 2   Q96FB6   Q96fb6 homo sapien
    17   49.5   56.2   1047 2   Q6ZRI6   Q6zri6 homo sapien
    18   49   55.7   182 2   Q6XQ03   Q6xq03 simian t-ly
    19   49   55.7   345 2   Q6RUK7   Q6ruk7 triticum mo
    20   49   55.7   401 1   OPRM_BOVIN   P79350 bos taurus

21	49	55.7	438	2	Q9Y2B5		Q9y2b5	homo sapien
22	49	55.7	476	2	Q88DD0		Q88dd0	pseudomonas
23	49	55.7	791	2	Q712J1		Q712j1	rattus norv
24	49	55.7	792	1	KFC2_MOUSE		O08672	mus musculu
25	48	54.5	321	2	Q9GRJ9		Q9grj9	leishmania
26	48	54.5	385	2	Q72H19		Q72h19	thermus the
27	48	54.5	409	2	Q6ZTV6		Q6ztv6	homo sapien
28	48	54.5	504	2	Q751U0		Q751u0	ashbya goss
29	48	54.5	652	2	O54859		O54859	rattus norv
30	48	54.5	744	2	O65375		O65375	arabidopsis
31	48	54.5	822	2	Q84LM0		Q84lm0	cucurbita m
32	47	53.4	235	2	Q8SV14		Q8sv14	encephalito
33	47	53.4	240	2	Q9YBV7		Q9ybv7	aeropyrum p
34	47	53.4	411	2	Q39554		Q39554	cuphea palu
35	47	53.4	574	2	Q9NVB3		Q9nvb3	homo sapien
36	47	53.4	678	2	Q84SH2		Q84sh2	oryza sativ
37	47	53.4	939	2	Q7SD71		Q7sd71	neurospora
38	47	53.4	1068	1	DAM2_MOUSE		Q80u19	mus musculu
39	47	53.4	1115	2	Q6TAB7		Q6tab7	mus musculu
40	47	53.4	1185	2	Q9NTD2		Q9ntd2	homo sapien
41	47	53.4	1329	2	Q86VY3		Q86vy3	homo sapien
42	47	53.4	1579	2	Q7QIP2		Q7qip2	anopheles g
43	47	53.4	1994	2	Q6ZPP2		Q6zpp2	mus musculu
44	47	53.4	2176	2	Q6V4S5		Q6v4s5	mus musculu
45	47	53.4	2217	2	Q8AV57		Q8av57	gallus gall